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U.S. DEPARTMENT OF COMMERCE
Patent and Trademark Office

SEARCH REQUEST FORM

Requestor's
Name:

BASKAR

Serial
Number:

10010160

Date:

9/30/03

Phone:

308-8886

Art Unit:

1645

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Claims 22-24

30-33

37-50

Seq. LD. No. 1

NA

ligu

interfer

40 hrs

Search:

NM 0016477

Accession rules

Lawsonia intracellularis
Vaccine

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Date completed:

10-08-03

Searcher:

Beverly C4974

Terminal time:

20 / 10

Elapsed time:

CPU time:

Total time:

25 / 22

Number of Searches:

Number of Databases:

2

Search Site

STIC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

IG

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other CEN

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Baskar P.
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(FILE 'HCAPLUS' ENTERED AT 12:36:01 ON 08 OCT 2003)

L1 103 SEA FILE=HCAPLUS ABB=ON PLU=ON (LAWSON? OR L) (W) INTRACE
LL?

L2 1 SEA FILE=HCAPLUS ABB=ON PLU=ON L1 AND (FLHB OR FLH B
OR PGTE? OR 16477)

L2 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:368499 HCAPLUS

DOCUMENT NUMBER: 136:382847

TITLE: Genes for antigenic proteins of Lawsonia and
their use diagnosis and prophylaxis of Lawsonia
infection

INVENTOR(S): Rosey, Everett Lee; King, Kendall Wayne; Good,
Robert Trygve; Strugnell, Richard Anthony

PATENT ASSIGNEE(S): Agriculture Victoria Services Pty. Ltd.,
Australia; Australian Pork Limited; Pfizer
Products, Inc.

SOURCE: PCT Int. Appl., 155 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---------------|--|----------|-----------------|----------|
| WO 2002038594 | A1 | 20020516 | WO 2001-AU1462 | 20011109 |
| WO 2002038594 | C2 | 20021107 | | |
| W: | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | |
| RW: | GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG | | | |
| AU 2002014810 | A5 | 20020521 | AU 2002-14810 | 20011109 |
| US 2003103999 | A1 | 20030605 | US 2001-10160 | 20011109 |
| BR 2001014835 | A | 20030701 | BR 2001-14835 | 20011109 |
| EP 1332154 | A1 | 20030806 | EP 2001-983297 | 20011109 |

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

PRIORITY APPLN. INFO.:

AU 2000-1381 A 20001110
US 2000-249596P P 20001117
WO 2001-AU1462 W 20011109

AB The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by **Lawsonia intracellularis** or similar or otherwise related microorganisms. In particular, the present invention provides a novel gene derived from **Lawsonia intracellularis**, which encodes an immunogenic polypeptide that is particularly useful as an antigen in a vaccine preparation for conferring humoral immunity against **Lawsonia intracellularis** and related pathogens in animal hosts, wherein said polypeptide is

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selected from the group consisting of **flhB**, **fliR**, **ntnC**, **glnH**, **motA**, **motB**, **tlyC**, **ytfM**, and **ytfN** polypeptides, or a homolog, analog or derivative of any one or more of said polypeptides. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 12:37:32 ON 08 OCT 2003)

L3

1 S L2

L3 ANSWER 1 OF 1 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2002-557448 [59] WPIDS

DOC. NO. NON-CPI: N2002-441304

DOC. NO. CPI: C2002-158153

TITLE: New immunogenic polypeptide comprising epitope of *Lawsonia* spp. polypeptide such as **flhB**, **fliR**, **ntnC**, **glnH**, **motA**, polypeptides, useful in vaccines for treatment of porcine proliferative enteropathy in pigs and birds.

DERWENT CLASS: B04 C06 D16 S03

INVENTOR(S): GOOD, R T; KING, K W; LEEROSEY, E; STRUGNELL, R A; ROSEY, E L

PATENT ASSIGNEE(S): (AGRI-N) AGRIC VICTORIA SERVICES PTY LTD; (AUPO-N) AUSTRALIAN PORK LTD; (PFIZ) PFIZER PROD INC; (GOOD-I) GOOD R T; (KING-I) KING K W; (ROSE-I) ROSEY E L; (STRU-I) STRUGNELL R A

COUNTRY COUNT: 99

PATENT INFORMATION:

| PATENT NO | KIND | DATE | WEEK | LA | PG |
|---|------|----------|-----------|----|-----|
| WO 2002038594 | A1 | 20020516 | (200259)* | EN | 155 |
| RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC | | | | | |
| MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW | | | | | |
| W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ | | | | | |
| DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP | | | | | |
| KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ | | | | | |
| NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA | | | | | |
| UG US UZ VN YU ZA ZW | | | | | |
| AU 2002014810 | A | 20020521 | (200260) | | |
| US 2003103999 | A1 | 20030605 | (200339) | | |
| EP 1332154 | A1 | 20030806 | (200353) | EN | |
| R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK | | | | | |
| NL PT RO SE SI TR | | | | | |
| BR 2001014835 | A | 20030701 | (200356) | | |

APPLICATION DETAILS:

| PATENT NO | KIND | APPLICATION | DATE |
|---------------|------|----------------|----------|
| WO 2002038594 | A1 | WO 2001-AU1462 | 20011109 |
| AU 2002014810 | A | AU 2002-14810 | 20011109 |

Searcher : Shears 308-4994

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|------------------------------|-----------------|----------|
| US 2003103999 A1 Provisional | US 2000-249595P | 20001117 |
| EP 1332154 A1 | US 2001-10160 | 20011109 |
| BR 2001014835 A | EP 2001-983297 | 20011109 |
| | WO 2001-AU1462 | 20011109 |
| | BR 2001-14835 | 20011109 |
| | WO 2001-AU1462 | 20011109 |

FILING DETAILS:

| PATENT NO | KIND | PATENT NO |
|-----------------|----------|---------------|
| AU 2002014810 A | Based on | WO 2002038594 |
| EP 1332154 A1 | Based on | WO 2002038594 |
| BR 2001014835 A | Based on | WO 2002038594 |

PRIORITY APPLN. INFO: US 2000-249596P 20001117; AU 2000-1381
20001110

AN 2002-557448 [59] WPIDS

AB WO 200238594 A UPAB: 20020916

NOVELTY - An isolated or recombinant immunogenic polypeptide (I) which comprises, mimics or cross-reacts with a B-cell or T-cell epitope of a *Lawsonia* spp. polypeptide such as fihB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM or ytfN polypeptides, is new.

DETAILED DESCRIPTION - An isolated or recombinant immunogenic polypeptide (I) which comprises, mimics or cross-reacts with a B-cell or T-cell epitope of a *Lawsonia* spp. polypeptide such as fihB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM or ytfN polypeptides, is:

(i) a polypeptide of *Lawsonia* spp. which comprises an amino acid sequence that has at least about 60% sequence identity overall to a fully defined amino acid (PS) sequence of 207 (S2), 262 (S4), 456 (S6), 137 (S8), 282 (S10), 237 (S12), 348 (S14), 602 (S16), or 1382 (S18) amino acids as given in specification;

(ii) a polypeptide of *Lawsonia* spp. which comprises an amino acid sequence which has at least 60% sequence identity overall to an amino acid sequence encoded by *L. intracellularis*

(Li) DNA contained within a plasmid (P) having AGAL Accession Nos:

NM00/16476 (plasmid **pGTE1** glnH); NM00/16477

(plasmid **pGTE2** flhB); NM00/16478 (plasmid

pGTE3 fliR); NM00/16479 (plasmid **pGTE4** motA/B);

NM00/16480 (plasmid **pGTE5** tlyC); NM00/16481 (plasmid

pGTE6 ntrC); NM00/16482 (plasmid **pGTE7** ytfM); or

NM01/23286 (plasmid **pGTE8** ytfN);

(iii) a polypeptide which comprises at least about 5 contiguous amino acids of PS;

(iv) a polypeptide which comprises at least about 5 contiguous amino acids of amino acid sequence of Li DNA contained within (P);

(v) a polypeptide which comprises an amino acid sequence encoded by nucleotide sequence of *Lawsonia* spp. having at least 60% identity overall to a fully defined nucleotide sequence (NS) of 622 (S1), 789 (S3), 1371 (S5), 412 (S7), 849 (S9), 717 (S11), 1047 (S13), 1812 (S15), or 4149 (S17) nucleotides as given in specification;

(vi) a polypeptide which comprises an amino acid sequence encoded by a nucleotide sequence of *Lawsonia* spp. having at least 60% sequence identity overall to nucleotide sequence of Li DNA contained within an (P);

(vii) a polypeptide encoded by at least 15 contiguous

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nucleotides of NS;

(viii) a polypeptide encoded by at least 15 contiguous nucleotides of nucleotide sequence of Li DNA contained within (P); or

(ix) a homolog, analog or derivative of above mentioned polypeptides which mimic a B-cell or T-cell epitope of *Lawsonia* spp.

INDEPENDENT CLAIMS are also included for the following:

(1) a vaccine composition (II) for the prophylaxis or treatment of infection of an animal by *Lawsonia* spp. which comprises an immunogenic component that comprises (I) and one or more carriers, diluents or adjuvants suitable for veterinary or pharmaceutical use;

(2) a combination vaccine composition (III) for the prophylaxis or treatment of infection of an animal by *Lawsonia* spp., comprising:

(i) a first immunogenic component which comprises (I); and

(ii) a second immunogenic component different from first immunogenic component and comprising a Li polypeptide such as FlgE, hemolysin, OmpH, SodC, **flhB**, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, or ytfN polypeptides and one or more carriers, diluents or adjuvants suitable for veterinary or pharmaceutical use;

(3) a vaccine vector (IV) that comprises, in an expressible form, an isolated nucleic acid molecule (V) comprising a nucleotide sequence such as:

(i) a protein-encoding nucleotide sequence having at least 60% sequence identity overall to a sequence of NS;

(ii) a protein-encoding nucleotide sequence having at least 60% identity overall to the protein-encoding sequence of Li DNA contained within (P);

(iii) a protein-encoding nucleotide sequence which comprises at least about 15 contiguous nucleotides of NS;

(iv) a protein-encoding nucleotide sequence which comprises at least 15 contiguous nucleotides of Li DNA contained within (P);

(v) a protein-encoding nucleotide sequence which hybridizes under low stringency condition to the complement of NS;

(vi) a protein-encoding nucleotide sequence which hybridizes under low stringency conditions to non-coding strand of Li DNA contained within (P); and

(vii) a homolog, analog or derivative of above mentioned nucleotide sequences which encodes the polypeptide that mimics a B-cell or T-cell epitope of *Lawsonia* spp.;

(4) an isolated polyclonal or monoclonal antibody molecule (VI) that binds specifically to *Lawsonia* spp. polypeptide of **flhB**, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, or ytfN polypeptide, or homolog, analog or derivative of the above mentioned polypeptide;

(5) an isolated nucleic acid molecule (N) which consists of a nucleotide sequence encoding *Lawsonia* spp. such as **flhB**, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, or ytfN;

(6) a probe or primer comprising any one of fully defined 50 oligonucleotide sequences as given in specification such as catattcaaggtacagcatctgatgg, ctctttacaaaccttgctcc, gctcatctaaagaacactttcc, caaggtagtatacaacttattgg, etc., or complementary nucleotide sequence to the oligonucleotide sequence;

(7) a plasmid having AGAL Accession Nos: NM00/16476 (plasmid **pGTE1** glnH); NM00/16477 (plasmid **pGTE2** **flhB**); NM00/16478 (plasmid **pGTE3** fliR); NM00/16479 (plasmid **pGTE4** motA/B); NM00/16480 (plasmid **pGTE5** tlyC); NM00/16481 (plasmid **pGTE6** ntrC); NM00/16482 (plasmid **pGTE7** ytfM); or NM01/23286 (plasmid **pGTE8**

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ytfn);

(8) a recombinant vector (VII) capable of replication in a host cell, where the vector comprises (N);

(9) a host cell (VIII) comprising (VII);

(10) identifying (M1) whether or not a porcine or avian animal has suffered from a past infection, or is currently infected, with Li or a microorganism that is immunologically cross-reactive with Li;

(11) diagnosing (M2) infection of a porcine or avian animal by Li or a microorganism that is immunologically cross-reactive with Li; and

(12) detecting (M3) Li or related microorganism in a biological sample derived from a porcine or avian animal subject.

ACTIVITY - Antibacterial.

MECHANISM OF ACTION - Vaccine. No supporting data is given.

USE - (I) is useful for identifying whether or not a porcine or avian animal has suffered from a past infection, or is currently infected, with Li or a microorganism that is immunologically cross-reactive with Li. (VI) is useful for diagnosing infection of a porcine or avian animal by Li or a microorganism that is immunologically cross-reactive with Li. (N) is useful as probes or primers for detecting Li or related microorganism in a biological sample derived from a porcine or avian animal subject (all claimed). (I) is preferably useful for vaccinating porcine animals against porcine proliferative enteropathy (PPE). (I) is also useful in vaccines for the prophylaxis and treatment of PPE in birds. (II) is useful for conferring protection against infection by other species of the genus Lawsonia or other microorganisms related to Li.

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FILE 'HCAPLUS' ENTERED AT 12:38:00 ON 08 OCT 2003

L4 0 S L1 AND NM0016477

FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 12:38:20 ON 08 OCT 2003

L5 0 S L4

(FILE 'HCAPLUS' ENTERED AT 12:38:37 ON 08 OCT 2003)

L1 103 SEA FILE=HCAPLUS ABB=ON PLU=ON (LAWSON? OR L) (W) INTRACE LL?

L6 1 SEA FILE=HCAPLUS ABB=ON PLU=ON L1 AND (16476 OR GLNH OR GLN H OR FLIR OR FLI R OR 16478 OR 16479 OR MOTA OR MOTB OR MOT OR MOTAB OR 16480 OR TLYC OR (NTR OR TLY) (W)C OR NTRC OR 16482 OR YTFM OR YTF(W) (M OR N) OR YTFN OR 23286)

L7 0 L6 NOT L2

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 12:42:26 ON 08 OCT 2003)

L8 1 S L6

L9 0 S L8 NOT L3

(FILE 'HCAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 12:44:05 ON 08 OCT 2003)

L10 112 S "ROSEY E"?/AU

L11 3959 S "KING K"?/AU

-Author (s)

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L12 7205 S "GOOD R"?/AU
L13 386 S "STRUGNELL R"?/AU
L14 2 S L10 AND L11 AND L12 AND L13
L15 14 S L10 AND (L11 OR L12 OR L13)
L16 2 S L11 AND (L12 OR L13)
L17 2 S L12 AND L13
L18 11644 S L10 OR L11 OR L12 OR L13
L19 18 S L18 AND L1
L20 30 S L14 OR L15 OR L16 OR L17 OR L19
L21 16 DUP REM L20 (14 DUPLICATES REMOVED)

L21 ANSWER 1 OF 16 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 2003:434075 BIOSIS
DOCUMENT NUMBER: PREV200300434075
TITLE: **Lawsonia intracellularis**
proteins, and related methods and materials.
AUTHOR(S): **Rosey, Everett L.**
ASSIGNEE: Pfizer, Inc.; Pfizer Products, Inc.
PATENT INFORMATION: US 6605696 August 12, 2003
SOURCE: Official Gazette of the United States Patent and
Trademark Office Patents, (Aug. 12 2003) Vol. 1273,
No. 2, pp. No. Pagination.
<http://www.uspto.gov/web/menu/patdata.html>. e-file.
ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English

AB Isolated polynucleotide molecules contain a nucleotide sequence that encodes a **L. intracellularis** HtrA, PonA, HypC, LysS, YcfW, ABC1, or Omp100 protein, a substantial portion of the sequences, or a homologous sequence. Related polypeptides, immunogenic compositions and assays are described.

L21 ANSWER 2 OF 16 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2003-416977 [39] WPIDS
DOC. NO. CPI: C2003-110367
TITLE: New isolated **Lawsonia intracellularis** polynucleotide and polypeptide, useful for the prevention and diagnosis of **Lawsonia** infections in susceptible animals, such as pigs.
DERWENT CLASS: B04 C06 D16
INVENTOR(S): **ROSEY, E L**
PATENT ASSIGNEE(S): (ROSE-I) ROSEY E L
COUNTRY COUNT: 1
PATENT INFORMATION:

| PATENT NO | KIND | DATE | WEEK | LA | PG |
|---------------|------|----------|-----------|----|----|
| US 2003021802 | A1 | 20030130 | (200339)* | | 64 |

APPLICATION DETAILS:

| PATENT NO | KIND | APPLICATION | DATE |
|---------------|------|-------------|--------------------------|
| US 2003021802 | A1 | Provisional | US 1999-160922P 19991022 |
| | | Provisional | US 1999-163858P 19991105 |
| | | Cont of | US 2000-689065 20001012 |

Searcher : Shears 308-4994

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US 2002-210296 20020801

PRIORITY APPLN. INFO: US 2002-210296 20020801; US 1999-160922P
19991022; US 1999-163858P 19991105; US
2000-689065 20001012

AN 2003-416977 [39] WPIDS

AB US2003021802 A UPAB: 20030619

NOVELTY - A new isolated polynucleotide molecule (I) comprises:

(a) a sequence encoding **Lawsonia intracellularis** HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein;

(b) a sequence that is a substantial part of the encoding sequence of (a); or

(c) a sequence homologous to the sequences of (a) or (b).

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a polynucleotide molecule comprising a nucleotide sequence greater than 20 nucleotides having promoter activity and found within a fully defined sequence of 5445 bp, given in the specification, from nucleotide 2691-2890, or its complement;

(2) a recombinant vector comprising (I);

(3) a transformed host cell comprising the vector of (2);

(4) a polypeptide produced by the transformed host cell of (3);

(5) a genetic construct comprising a polynucleotide molecule that can be used to alter a **Lawsonia** gene, comprising: (a) polynucleotide molecule comprising a sequence that is otherwise the same as a nucleotide sequence of a htrA, ponA, hypC, lysS, ycfW, abcl or omp100 gene, or its homolog, substantial portion, or mutations capable of altering the above mentioned genes; or (b) a polynucleotide molecule comprising a sequence that naturally flanks in situ the ORF of the htrA, ponA, hypC, lysS, ycfW, abcl or omp100 gene, or its homolog;

(6) a transformed host cell comprising the genetic construct of (5);

(7) an isolated polypeptide comprising: (a) a **Lawsonia intracellularis** HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein; (b) homologs or substantial portions of (a); (c) a fusion protein of the polypeptide in (a) or (b) fused to another protein or polypeptide; or (d) an analog or derivative of the polypeptide in (a), (b) or (c);

(8) a substantially pure polypeptide comprising an epitope of HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein that is specifically reactive with anti-**Lawsonia** antibodies;

(9) an isolated polypeptide comprising the sequence encoded by (I);

(10) an isolated antibody that specifically reacts with **L. intracellularis** HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein;

(11) a live attenuated vaccine comprising the transformed cell of (6);

(12) a killed cell vaccine comprising transformed cells of (6) in killed form; and

(13) an immunogenic composition comprising (I) or the polypeptide of (7), in combination with a carrier.

ACTIVITY - Antibacterial. No biological data given.

MECHANISM OF ACTION - Vaccine.

USE - The methods and compositions of the present invention are

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useful for the prevention and diagnosis of **L. intracellularis** infections in susceptible animals, such as pigs.
Dwg.0/9

L21 ANSWER 3 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2002:368499 HCAPLUS
DOCUMENT NUMBER: 136:382847
TITLE: Genes for antigenic proteins of Lawsonia and their use diagnosis and prophylaxis of Lawsonia infection
INVENTOR(S): Rosey, Everett Lee; King, Kendall Wayne; Good, Robert Trygve; Strugnell, Richard Anthony
PATENT ASSIGNEE(S): Agriculture Victoria Services Pty. Ltd., Australia; Australian Pork Limited; Pfizer Products, Inc.
SOURCE: PCT Int. Appl., 155 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------------------|---|----------|-----------------|------------|
| WO 2002038594 | A1 | 20020516 | WO 2001-AU1462 | 20011109 |
| WO 2002038594 | C2 | 20021107 | | |
| W: | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | |
| RW: | GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG | | | |
| AU 2002014810 | A5 | 20020521 | AU 2002-14810 | 20011109 |
| US 2003103999 | A1 | 20030605 | US 2001-10160 | 20011109 |
| BR 2001014835 | A | 20030701 | BR 2001-14835 | 20011109 |
| EP 1332154 | A1 | 20030806 | EP 2001-983297 | 20011109 |
| R: | AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR | | | |
| PRIORITY APPLN. INFO.: | | | AU 2000-1381 | A 20001110 |
| | | | US 2000-249596P | P 20001117 |
| | | | WO 2001-AU1462 | W 20011109 |
| AB | The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by Lawsonia intracellularis or similar or otherwise related microorganisms. In particular, the present invention provides a novel gene derived from Lawsonia intracellularis , which encodes an immunogenic polypeptide that is particularly useful as an antigen in a vaccine preparation for conferring humoral immunity against Lawsonia intracellularis and related pathogens in animal hosts, wherein said polypeptide is | | | |

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selected from the group consisting of flhB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, and ytfN polypeptides, or a homolog, analog or derivative of any one or more of said polypeptides. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 4 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 2002:752377 HCAPLUS
DOCUMENT NUMBER: 137:277776
TITLE: Sequences of Mycoplasma hyopneumoniae antigen mhp3 and therapeutic and diagnosis uses
INVENTOR(S): King, Kendall Wayne; Madura, Rebecca Anne; Rosey, Everett Lee
PATENT ASSIGNEE(S): Pfizer Products Inc., USA
SOURCE: Eur. Pat. Appl., 38 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|------|----------|-----------------|------------|
| EP 1245677 | A1 | 20021002 | EP 2001-303030 | 20010330 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR | | | | |
| BR 2001002541 | A | 20020528 | BR 2001-2541 | 20010329 |
| JP 2002306169 | A2 | 20021022 | JP 2001-101364 | 20010330 |
| PRIORITY APPLN. INFO.: | | | US 2000-676249 | A 20000929 |
| | | | EP 2001-303030 | A 20010330 |

AB The present invention provides protein and DNA sequences of Mycoplasma hyopneumoniae antigen mhp3 gene. The present invention further relates to novel apoprotein antigens encoded by mhp3 gene for use in vaccines to prevent and treat diseases caused by infection with Mycoplasma hyopneumoniae. The invention further relates to methods, vector and host cells for recombinant production of such antigens. The invention also relates to diagnosis of infections in pig caused by Mycoplasma hyopneumoniae.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 5 OF 16 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN
ACCESSION NUMBER: 2002-609319 [66] WPIDS
DOC. NO. CPI: C2002-172381
TITLE: Nucleic acids and proteins of gene MHP3 of Mycoplasma hyopneumoniae are used in vaccines for prophylaxis and treatment of infections caused by Mycoplasma hyopneumoniae.
DERWENT CLASS: B04 S03
INVENTOR(S): KING, K W; MADURA, R A; ROSEY, E
L

Searcher : Shears 308-4994

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10/010160

PATENT ASSIGNEE(S): (PFIZ) PFIZER INC
COUNTRY COUNT: 1
PATENT INFORMATION:

| PATENT NO | KIND | DATE | WEEK | LA | PG |
|---------------|------|----------|-----------|----|----|
| BR 2001002541 | A | 20020528 | (200266)* | | 1 |

APPLICATION DETAILS:

| PATENT NO | KIND | APPLICATION | DATE |
|---------------|------|--------------|----------|
| BR 2001002541 | A | BR 2001-2541 | 20010329 |

PRIORITY APPLN. INFO: US 2000-676249 20000929

AN 2002-609319 [66] WPIDS

AB BR 200102541 A UPAB: 20021014

NOVELTY - Nucleic acids and proteins of the gene MHP3 of Mycoplasma hyopneumoniae are used in vaccines for prophylaxis and treatment of infections caused by Mycoplasma hyopneumoniae.

USE - In the prevention and treatment of illnesses caused by infections by Mycoplasma hyopneumoniae.
Dwg.0/0

L21 ANSWER 6 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 3

ACCESSION NUMBER: 2001:261139 HCAPLUS

DOCUMENT NUMBER: 134:294510

TITLE: Sequences of Mycoplasma hyopneumoniae antigen mhp3 and therapeutic uses thereof

INVENTOR(S): **King, Kendall Wayne**; Madura, Rebecca
Anne; **Rosey, Everett Lee**

PATENT ASSIGNEE(S): Pfizer Products Inc., USA

SOURCE: Eur. Pat. Appl., 38 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------|------|----------|-----------------|----------|
| EP 1090995 | A2 | 20010411 | EP 2000-308421 | 20000926 |
| EP 1090995 | A3 | 20010418 | | |

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, SI, LT, LV, FI, RO

| | | | | |
|---------------|---|----------|--------------|----------|
| BR 2000004488 | A | 20011113 | BR 2000-4488 | 20000927 |
|---------------|---|----------|--------------|----------|

| | | | | |
|-----------|---|----------|----------------|----------|
| NZ 507205 | A | 20020301 | NZ 2000-507205 | 20000928 |
|-----------|---|----------|----------------|----------|

| | | | | |
|------------|---|----------|----------------|----------|
| CN 1296953 | A | 20010530 | CN 2000-129083 | 20000929 |
|------------|---|----------|----------------|----------|

| | | | | |
|---------------|----|----------|----------------|----------|
| JP 2001149085 | A2 | 20010605 | JP 2000-300778 | 20000929 |
|---------------|----|----------|----------------|----------|

PRIORITY APPLN. INFO.: US 1999-156602P P 19990929

AB The present invention provides protein and DNA sequences of Mycoplasma hyopneumoniae antigen mhp3 gene. The present invention further relates to novel apoprotein antigens encoded by mhp3 gene for use in vaccines to prevent and treat diseases caused by infection with Mycoplasma hyopneumoniae. The invention further relates to method recombinant production of such antigens.

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L21 ANSWER 7 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:297553 HCAPLUS

DOCUMENT NUMBER: 134:321599

TITLE: Cloning of Lawsonia genes htrA, ponA, hypC, lysS, ycfW, abcl, and omp100, their encoded proteins or peptides and therapeutic use in diagnosis and as vaccine

INVENTOR(S): Rosey, Everett Lee

PATENT ASSIGNEE(S): Pfizer Products Inc., USA

SOURCE: Eur. Pat. Appl., 80 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|------|----------|-----------------|-------------|
| EP 1094070 | A2 | 20010425 | EP 2000-309125 | 20001017 |
| EP 1094070 | A3 | 20020109 | | |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | | |
| US 6605696 | B1 | 20030812 | US 2000-689065 | 20001012 |
| JP 2001169787 | A2 | 20010626 | JP 2000-320736 | 20001020 |
| US 2003021802 | A1 | 20030130 | US 2002-210296 | 20020801 |
| PRIORITY APPLN. INFO.: | | | US 1999-160922P | P 19991022 |
| | | | US 1999-163868P | P 19991105 |
| | | | US 2000-689065 | A1 20001012 |

AB The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in pigs or other animals caused or exacerbated by **Lawsonia intracellularis** or similar or otherwise related microorganism, such as porcine proliferative enteropathy (PPE). In particular, the present invention provides novel genes htrA, ponA, hypC, lysS, ycfW, abcl, and omp100 derived from **Lawsonia intracellularis** genomic regions A and B. These genes encode sequence homologs to lysyl-tRNA synthetase (gene lysS), transmembrane or integral membrane protein (abcl), hydrogenase maturation protein (hypC), penicillin binding protein (ponA), and periplasmic serine protease protein (htrA) resp. The invention also relates to constructing these gene expression vector to produce recombinant protein using E. coli. Methods of expressing recombinant htrA and omp100 proteins in E. coli are also provided. The invention also provides the immunogenic peptides or proteins encoded by these genes that are particularly useful as an antigen in vaccine preparation for conferring humoral immunity against **Lawsonia intracellularis** and related pathogens in animal hosts. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

L21 ANSWER 8 OF 16 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2001-592540 [67] WPIDS

DOC. NO. NON-CPI: N2001-441503

DOC. NO. CPI: C2001-175788

TITLE: **Lawsonia intracellularis**

Searcher : Shears 308-4994

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polynucleotide and encoded protein, used to prevent
Lawsonia intracellularis
infection.

DERWENT CLASS: B04 C06 D16 S03
INVENTOR(S): ROSEY, E L
PATENT ASSIGNEE(S): (PFIZ) PFIZER PROD INC
COUNTRY COUNT: 26
PATENT INFORMATION:

| PATENT NO | KIND | DATE | WEEK | LA | PG |
|--|------|----------|-----------|----|----|
| JP 2001169787 | A | 20010626 | (200167)* | | 67 |
| EP 1094070 | A2 | 20010425 | (200167) | EN | |
| R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI | | | | | |

APPLICATION DETAILS:

| PATENT NO | KIND | APPLICATION | DATE |
|---------------|------|----------------|----------|
| JP 2001169787 | A | JP 2000-320736 | 20001020 |
| EP 1094070 | A2 | EP 2000-309125 | 20001017 |

PRIORITY APPLN. INFO: US 1999-160922P 19991022

AN 2001-592540 [67] WPIDS

AB JP2001169787 A UPAB: 20011129

NOVELTY - An isolated polynucleotide molecule containing a nucleotide sequence encoding HtrA, PonA, HypC, LysS, YefW, ABC1 or Omp100 protein of **Lawsonia intracellularis**, or it's fragment or homolog, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) polynucleotide molecule containing more than 20 nucleotides having promotor activity and being found in nucleotides 2691-2890 of a 5445 nucleotide sequence, fully defined in the specification, or its complement;

(2) a recombinant vector containing the polynucleotide of (1);

(3) a transformed host cell transformed containing the novel vector;

(4) a polypeptide produced by the cell of (3);

(5) a gene construct containing a polynucleotide molecule which can be used for changing *Lawsonia* gene;

(6) a transformed cell containing the construct of (5);

(7) an isolated polypeptide produced by the cell of (6);

(8) an attenuated live vaccine containing the transformed cell of (6);

(9) a killed vaccine containing the cell of (6) in dead form; and

(10) an immunogenic composition containing an immunologically effective amount of the polypeptide of (3), and a carrier.

ACTIVITY - Antibacterial.

No biological data is given.

MECHANISM OF ACTION - Vaccine.

USE - The composition is useful for the prevention of **Lawsonia intracellularis** infection.

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L21 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 2000:824297 HCAPLUS
DOCUMENT NUMBER: 134:1364
TITLE: Lawsonia-derived gene tlyA and related hemolysin
polypeptides, peptides and proteins and their
uses for diagnosis and treatment of avian and
porcine infections
INVENTOR(S): Panaccio, Michael; Rosey, Everett Lee;
Hasse, Detlef; Ankenbauer, Robert Gerard
PATENT ASSIGNEE(S): Pfizer Products Inc, USA; Agriculture Victoria
Services Pty Ltd; Pig Research and Development
Corporation
SOURCE: PCT Int. Appl., 86 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------------------|--|----------|-------------------|----------|
| WO 2000069906 | A1 | 20001123 | WO 2000-AU439 | 20000511 |
| W: | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | |
| RW: | GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | |
| EP 1177213 | A1 | 20020206 | EP 2000-924978 | 20000511 |
| R: | AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | |
| NZ 515363 | A | 20030725 | NZ 2000-515363 | 20000511 |
| PRIORITY APPLN. INFO.: | | | US 1999-134022P P | 19990513 |
| | | | WO 2000-AU439 W | 20000511 |

AB The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by **Lawsonia intracellularis** or similar or otherwise related microorganism. In particular, the present invention provides a novel gene derived from **Lawsonia intracellularis** which encodes an immunogenic TylA hemolysin peptide, polypeptide or protein that is particularly useful as an antigen in vaccine preparation for conferring humoral immunity against **Lawsonia intracellularis** and related pathogens in animal hosts. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 10 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 5
ACCESSION NUMBER: 2000:824295 HCAPLUS

Searcher : Shears 308-4994

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DOCUMENT NUMBER: 133:359825
TITLE: Lawsonia-derived gene flgE and related flagellar hook polypeptides, peptides and proteins and their uses for diagnosis and treatment of avian and porcine infections
INVENTOR(S): Panaccio, Michael; Rosey, Everett Lee; Sinistaj, Meri; Hasse, Detlef; Parsons, Jim; Ankenbauer, Robert Gerard
PATENT ASSIGNEE(S): Pfizer Products Inc., USA; Agriculture Victoria Services Pty Ltd; Pig Research and Development Corporation
SOURCE: PCT Int. Appl., 97 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------------------|--|----------|-------------------|----------|
| WO 2000069904 | A1 | 20001123 | WO 2000-AU437 | 20000511 |
| W: | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | |
| RW: | GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | |
| BR 2000011294 | A | 20020226 | BR 2000-11294 | 20000511 |
| EP 1181315 | A1 | 20020227 | EP 2000-924976 | 20000511 |
| R: | AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | |
| JP 2003516113 | T2 | 20030513 | JP 2000-618320 | 20000511 |
| NZ 515331 | A | 20030725 | NZ 2000-515331 | 20000511 |
| US 2003157120 | A1 | 20030821 | US 2002-9823 | 20020813 |
| PRIORITY APPLN. INFO.: | | | US 1999-133973P P | 19990513 |
| | | | WO 2000-AU437 W | 20000511 |

AB The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by **Lawsonia intracellularis** or similar or otherwise related microorganism. In particular, the present invention provides a novel gene derived from **Lawsonia intracellularis** which encodes an immunogenic FlgE flagellar hook peptide, polypeptide or protein that is particularly useful as an antigen in vaccine preparation for conferring humoral immunity against **Lawsonia intracellularis** and related pathogens in animal hosts. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L21 ANSWER 11 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 6
ACCESSION NUMBER: 2000:824294 HCAPLUS
DOCUMENT NUMBER: 133:359824
TITLE: Lawsonia-derived gene sodC and related
superoxide dismutase polypeptides, peptides and
proteins and their uses for diagnosis and
treatment of avian and porcine infections
INVENTOR(S): Ankenbauer, Robert Gerard; Hasse, Detlef;
Panaccio, Michael; **Rosey, Everett Lee**;
Wright, Catherine
PATENT ASSIGNEE(S): Pfizer Products, Inc., USA; Pig Research and
Development Corp.; Agriculture Victoria Services
Pty., Ltd.
SOURCE: PCT Int. Appl., 85 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------------------|--|----------|-------------------|----------|
| WO 2000069903 | A1 | 20001123 | WO 2000-AU436 | 20000511 |
| W: | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | |
| RW: | GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | |
| EP 1177212 | A1 | 20020206 | EP 2000-924975 | 20000511 |
| R: | AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | |
| BR 2000011292 | A | 20020226 | BR 2000-11292 | 20000511 |
| JP 2003501013 | T2 | 20030114 | JP 2000-618319 | 20000511 |
| PRIORITY APPLN. INFO.: | | | US 1999-133989P P | 19990513 |
| | | | WO 2000-AU436 W | 20000511 |

AB The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by **Lawsonia intracellularis** or similar or otherwise related microorganism. In particular, the present invention provides a novel gene derived from **Lawsonia intracellularis** which encodes an immunogenic SodC superoxide dismutase peptide, polypeptide or protein that is particularly useful as an antigen in vaccine preparation for conferring humoral immunity against **Lawsonia intracellularis** and related pathogens in animal hosts. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L21 ANSWER 12 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 7
ACCESSION NUMBER: 1998:558037 HCAPLUS
DOCUMENT NUMBER: 129:255827
TITLE: Identification and sequencing of the groE operon
and flanking genes of **Lawsonia**
intracellularis: use in phylogeny
AUTHOR(S): Dale, C. Jane H.; Moses, Eric K.; Ong,
Chin-Chui; Morrow, Chris J.; Reed, Michael B.;
Hasse, Dete; **Strugnell, Richard A.**
CORPORATE SOURCE: Victorian Institute of Animal Science, Victoria,
3049, Australia
SOURCE: Microbiology (Reading, United Kingdom) (1998),
144(8), 2073-2084
CODEN: MROBEO; ISSN: 1350-0872
PUBLISHER: Society for General Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Proliferative enteropathy (PE) is a complex of diseases of com.
importance to the pig industry. The obligate intracellular
bacterium **Lawsonia intracellularis** is
consistently associated with PE and pure cultures of this bacterium
have been used to reproduce PE in pigs. In this study **L.**
intracellularis bacteria were purified directly from
PE-affected tissue. DNA extracted from purified bacteria was used to
construct a partial genomic library which was screened using sera
from **L. intracellularis**-immunized rabbits. Two
seroreactive recombinant clones were identified, one of which
expressed proteins of 10 and 60 kDa. The sequence of the insert
from this clone, pISI-2, revealed ORFs with sequence similarity to
the groES/EL operon of *Escherichia coli*, the 50S ribosomal proteins
L21 and L27 of *E. coli*, a GTP-binding protein of *Bacillus subtilis*
and a possible protoporphyrinogen oxidase, HemK, of *E. coli*.
Primers designed from unique sequences from the pISI-2 insert
amplified DNA from infected, but not non-infected, porcine ilea; the
amplicon sequence obtained from tissue-cultured **L.**
intracellularis was identical to the corresponding sequence
in pISI-2, confirming the origin of the clone. The sequence of
L. intracellularis GroEL and other GroEL sequences
in the databases were used to construct a partial phylogenetic tree.
Anal. of the GroEL sequence relationship suggested that **L.**
intracellularis is not significantly related to other
organisms whose GroEL sequences are held in the databases and
supports previous data from 16S sequence analyses suggesting that
L. intracellularis is a member of a novel group of
enteric pathogens.
REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L21 ANSWER 13 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 8
ACCESSION NUMBER: 1997:171184 HCAPLUS
DOCUMENT NUMBER: 126:224028
TITLE: Characterization of the gene encoding Mhp1 from
Mycoplasma hyopneumoniae and examination of
Mhp1's vaccine potential
AUTHOR(S): King, Kendall W.; Faulds, Daryl H.;
Rosey, Everett L.; Yancey, Robert J.,
Jr.

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10/010160

CORPORATE SOURCE: Veterinary Infectious Disease, The Upjohn
Company, Kalamazoo, MI, 49001, USA
SOURCE: Vaccine (1997), 15(1), 25-35
CODEN: VACCDE; ISSN: 0264-410X
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The gene encoding Mhp1, a 124-kDa protein from Mycoplasma hyopneumoniae, has been cloned, sequenced, and its product characterized. No significant homol. to the gene or encoded polypeptide was found in the Genbank, NBRF, or PIR databases, though this protein appears similar to p97, a putative adhesin of M. hyopneumoniae. Two repeated motifs were identified within the 3' end of the gene and encoded polypeptide. The mhp1 gene was fused to the glutathione S-transferase (GST) gene from Schistosoma japonicum, enabling high-level expression and purification of the protein. Both the authentic and recombinant proteins were recognized by sera from pigs infected with M. hyopneumoniae. In an induced-disease model in pigs, coughing was reduced in animals vaccinated with recombinant GST-Mhp1, although differences were not significant. Only minimal protection against lung lesion formation was provided, and again differences between the Mhp1-vaccinated and nonvaccinated groups were not significant.

L21 ANSWER 14 OF 16 JAPIO (C) 2003 JPO on STN
ACCESSION NUMBER: 2002-306169 JAPIO
TITLE: NUCLEIC ACID OF MHP3 GENE OF MYCOPLASMA
HYOPNEUMONIAE, PROTEIN ENCODED BY THE GENE, AND
THEIER USES
INVENTOR: KING KENDALL WAYNE; MADURA REBECCA
ANNE; ROSEY EVERETT LEE
PATENT ASSIGNEE(S): PFIZER PROD INC
PATENT INFORMATION:

| PATENT NO | KIND | DATE | ERA | MAIN IPC |
|---------------|------|----------|--------|------------|
| JP 2002306169 | A | 20021022 | Heisei | C12N015-09 |

APPLICATION INFORMATION

STN FORMAT: JP 2001-101364 20010330
ORIGINAL: JP2001101364 Heisei
PRIORITY APPLN. INFO.: JP 2001-101364 20010330
SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined
Applications, Vol. 2002

AN 2002-306169 JAPIO

AB PROBLEM TO BE SOLVED: To provide a nucleic acid of mhp3 gene of Mycoplasma hyopneumoniae and a protein encoded by the gene.
SOLUTION: A new apoprotein encoded by mhp3 gene used in a vaccine for preventing and treating a disease caused by Mycoplasma hyopneumoniae and a method for producing the above antigen by the recombination, are provided.
COPYRIGHT: (C)2002,JPO

L21 ANSWER 15 OF 16 JAPIO (C) 2003 JPO on STN
ACCESSION NUMBER: 2001-169787 JAPIO
TITLE: LAWSONIA INTRACELLULARIS
PROTEIN, RELEVANT METHOD AND MATERIAL
INVENTOR: ROSEY EVERETT LEE

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PATENT ASSIGNEE(S): PFIZER PROD INC
PATENT INFORMATION:

| PATENT NO | KIND | DATE | ERA | MAIN IPC |
|---------------|------|----------|--------|------------|
| JP 2001169787 | A | 20010626 | Heisei | C12N015-09 |

APPLICATION INFORMATION

STN FORMAT: JP 2000-320736 20001020
ORIGINAL: JP2000320736 Heisei
PRIORITY APPLN. INFO.: US 1999-160922 19991022
SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined
Applications, Vol. 2001

AN 2001-169787 JAPIO

AB PROBLEM TO BE SOLVED: To isolate a **Lawsonia intracellularis** protein, and to provide a relevant method and a material.

SOLUTION: The isolated polypeptide molecule includes a nucleotide sequence encoding **L. intracellularis** htrA, ponA, hypC, lysS, ycfW, abcl or omp100 protein, a substantial part in the nucleotide sequence or its homologous sequence. Relevant polypeptides, immunogenic compositions and methods for assay are described.

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L21 ANSWER 16 OF 16 JAPIO (C) 2003 JPO on STN

ACCESSION NUMBER: 2001-149085 JAPIO

TITLE: NUCLEIC ACID OF mhp3 GENE OF Mycoplasma hyopneumoniae, PROTEIN ENCODED BY THE GENE, AND USES THEREOF

INVENTOR: KING KENDALL WAYNE; MADURA REBECCA ANNE; ROSEY EVERETT LEE

PATENT ASSIGNEE(S): PFIZER PROD INC
PATENT INFORMATION:

| PATENT NO | KIND | DATE | ERA | MAIN IPC |
|---------------|------|----------|--------|------------|
| JP 2001149085 | A | 20010605 | Heisei | C12N015-09 |

APPLICATION INFORMATION

STN FORMAT: JP 2000-300778 20000929
ORIGINAL: JP2000300778 Heisei
PRIORITY APPLN. INFO.: US 1999-156602 19990929
SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined
Applications, Vol. 2001

AN 2001-149085 JAPIO

AB PROBLEM TO BE SOLVED: To obtain Mycoplasma hyopneumoniae mhp3 gene nucleic acid and a protein encoded by the nucleic acid.

SOLUTION: A new apoprotein antigen is provided which is encoded by mhp3 used in vaccine for preventing and treating a disease caused by the infection of Mycoplasma hyopneumoniae. A method for producing the antigen by the recombination is also provided.

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FILE 'HOME' ENTERED AT 12:46:16 ON 08 OCT 2003

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 05:12:07 ; Search time 2003 Seconds

(without alignments)
12703.838 Million cell updates/sec

Title: US-10-010-160-1

Perfect score: 622

Sequence: 1 atgtcgtatgaccaccagta.....aattatgcagtcgcagatc 622

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl.*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 22 | 3.5 | 108534 | 2 | AL021327 Human DNA |
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| 4 | 22 | 3.5 | 138519 | 2 | AL135926 Human DNA |
| 5 | 22 | 3.5 | 160961 | 2 | AC141118 Ratrus no |
| 6 | 22 | 3.5 | 164604 | 2 | BX296535 Dantio rer |
| 7 | 22 | 3.5 | 183901 | 2 | AL356425 Homo sapi |
| 8 | 22 | 3.5 | 250935 | 2 | AC135412 Ratrus no |
| 9 | 22 | 3.5 | 286790 | 2 | AC096515 Ratrus no |
| 10 | 22 | 3.4 | 44284 | 2 | AC013856 Drosophila |
| 11 | 21 | 3.4 | 60164 | 2 | AC020373 Drosophila |
| 12 | 21 | 3.4 | 61913 | 9 | AL671966 Human DNA |
| 13 | 21 | 3.4 | 82517 | 9 | HS341D10 |
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| 15 | 21 | 3.4 | 127641 | 9 | AL354827 Human DNA |
| 16 | 21 | 3.4 | 147078 | 2 | AC080184 |
| 17 | 21 | 3.4 | 151802 | 2 | AC114263 |
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| 19 | 21 | 3.4 | 164018 | 10 | AL646050 Mouse DNA |
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| 24 | 21 | 3.4 | 174902 | 2 | AC110071 |
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| 28 | 21 | 3.4 | 194036 | 9 | AC091388 Drosophila |
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| 31 | 21 | 3.4 | 198088 | 9 | AC078957 Homo sapi |
| 32 | 21 | 3.4 | 215435 | 2 | AC126275 |
| 33 | 21 | 3.4 | 216734 | 5 | AB073376 Oryzias l |
| 34 | 21 | 3.4 | 218708 | 2 | AC021166 Homo sapi |
| 35 | 21 | 3.4 | 226584 | 2 | AC145044 Bos tauru |
| 36 | 21 | 3.4 | 254050 | 3 | PPA929358 Plasmodu |
| 37 | 21 | 3.4 | 256227 | 3 | AE003827 Drosophila |
| 38 | 21 | 3.4 | 259474 | 3 | HUAC004605 |
| 39 | 21 | 3.4 | 265215 | 3 | AE003837 Drosophila |
| 40 | 20 | 3.2 | 172 | 3 | DROMTMR2 |
| 41 | 20 | 3.2 | 191 | 3 | DROMTMR2 |
| 42 | 20 | 3.2 | 237 | 3 | DAU94254 |
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| 44 | 20 | 3.2 | 237 | 3 | DAU94259 |
| 45 | 20 | 3.2 | 237 | 3 | DAU94261 |
| 46 | 20 | 3.2 | 237 | 3 | DAU94264 |
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| 65 | 20 | 3.2 | 610 | 3 | DMU07318 |
| 66 | 20 | 3.2 | 610 | 3 | DPU07322 |

Pred. No. is the number of results predicted by chance to have a

| | | | | | | | | | | | | | | | |
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| C 66 | 20 | 3.2 | 610 | 3 | DP007328 | U07328 | Drosophila | C 139 | 20 | 3.2 | 14916 | 3 | AF200829 | AF200829 | Drosophila |
| C 67 | 20 | 3.2 | 610 | 3 | DTU07306 | U07306 | Drosophila | C 140 | 20 | 3.2 | 14943 | 3 | AF200886 | AF200886 | Drosophila |
| C 68 | 20 | 3.2 | 634 | 3 | AF246504 | AF246504 | Drosophila | C 141 | 20 | 3.2 | 14943 | 3 | AF200887 | AF200887 | Drosophila |
| C 69 | 20 | 3.2 | 642 | 3 | AF246503 | AF246503 | Drosophila | C 142 | 20 | 3.2 | 14943 | 3 | AF200888 | AF200888 | Drosophila |
| C 70 | 20 | 3.2 | 678 | 3 | AF479797 | AF479797 | Drosophila | C 143 | 20 | 3.2 | 14943 | 3 | AF200889 | AF200889 | Drosophila |
| C 71 | 20 | 3.2 | 680 | 3 | AF246515 | AF246515 | Drosophila | C 144 | 20 | 3.2 | 14943 | 3 | AF200890 | AF200890 | Drosophila |
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| C 77 | 20 | 3.2 | 691 | 3 | AF246502 | AF246502 | Drosophila | C 150 | 20 | 3.2 | 14945 | 3 | AF200882 | AF200882 | Drosophila |
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| C 83 | 20 | 3.2 | 692 | 3 | AF246508 | AF246508 | Drosophila | C 156 | 20 | 3.2 | 14946 | 3 | AF200885 | AF200885 | Drosophila |
| C 84 | 20 | 3.2 | 692 | 3 | AF246509 | AF246509 | Drosophila | C 157 | 20 | 3.2 | 14950 | 3 | AF200882 | AF200882 | Drosophila |
| C 85 | 20 | 3.2 | 692 | 3 | AF246510 | AF246510 | Drosophila | C 158 | 20 | 3.2 | 14964 | 3 | AF200830 | AF200830 | Drosophila |
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| C 87 | 20 | 3.2 | 692 | 3 | AF246513 | AF246513 | Drosophila | C 160 | 20 | 3.2 | 14970 | 3 | AF200837 | AF200837 | Drosophila |
| C 88 | 20 | 3.2 | 692 | 3 | AF246516 | AF246516 | Drosophila | C 161 | 20 | 3.2 | 14972 | 3 | AF200833 | AF200833 | Drosophila |
| C 89 | 20 | 3.2 | 692 | 3 | AF246517 | AF246517 | Drosophila | C 162 | 20 | 3.2 | 14973 | 3 | AF200835 | AF200835 | Drosophila |
| C 90 | 20 | 3.2 | 692 | 3 | AF246518 | AF246518 | Drosophila | C 163 | 20 | 3.2 | 14973 | 3 | AF200836 | AF200836 | Drosophila |
| C 91 | 20 | 3.2 | 692 | 3 | AF246519 | AF246519 | Drosophila | C 164 | 20 | 3.2 | 14974 | 3 | AF200834 | AF200834 | Drosophila |
| C 92 | 20 | 3.2 | 693 | 3 | AF246495 | AF246495 | Drosophila | C 165 | 20 | 3.2 | 16019 | 3 | MYDIRRN | MYDIRRN | Drosophila |
| C 93 | 20 | 3.2 | 694 | 3 | AF246498 | AF246498 | Drosophila | C 166 | 20 | 3.2 | 21915 | 3 | DMU37551 | DMU37551 | Drosophila |
| C 94 | 20 | 3.2 | 694 | 3 | AF479810 | AF479810 | Paranyctop | C 167 | 20 | 3.2 | 21915 | 1 | AE008824 | AE008824 | Salmonella |
| C 95 | 20 | 3.2 | 695 | 3 | AF246511 | AF246511 | Drosophila | C 168 | 20 | 3.2 | 63823 | 2 | AC114647 | AC114647 | Mus musculus |
| C 96 | 20 | 3.2 | 713 | 3 | AF536639 | AF536639 | Cryptococ | C 169 | 20 | 3.2 | 73477 | 9 | AC108668 | AC108668 | Homo sapiens |
| C 97 | 20 | 3.2 | 713 | 3 | AF536640 | AF536640 | Cryptococ | C 170 | 20 | 3.2 | 74048 | 2 | AC1015895 | AC1015895 | Homo sapiens |
| C 98 | 20 | 3.2 | 716 | 3 | AF479809 | AF479809 | Mycoctroso | C 171 | 20 | 3.2 | 82875 | 8 | AC013482 | AC013482 | Genomic s |
| C 99 | 20 | 3.2 | 736 | 3 | AF059892 | AF059892 | Drosophila | C 172 | 20 | 3.2 | 83408 | 8 | AB078516 | AB078516 | Arabidops |
| C 100 | 20 | 3.2 | 741 | 3 | AF479805 | AF479805 | Drosophila | C 173 | 20 | 3.2 | 89737 | 8 | AC027036 | AC027036 | Arabidops |
| C 101 | 20 | 3.2 | 742 | 3 | AF479811 | AF479811 | Samoaia 1 | C 174 | 20 | 3.2 | 93929 | 2 | AC110967_3 | AC110967_3 | Continuatio |
| C 102 | 20 | 3.2 | 745 | 3 | AF479807 | AF479807 | Drosophila | C 175 | 20 | 3.2 | 95581 | 8 | AC015448 | AC015448 | Arabidops |
| C 103 | 20 | 3.2 | 746 | 3 | AF479802 | AF479802 | Drosophila | C 176 | 20 | 3.2 | 96936 | 8 | ATP8F6 | ATP8F6 | Arabidops |
| C 104 | 20 | 3.2 | 750 | 3 | AF479808 | AF479808 | Drosophila | C 177 | 20 | 3.2 | 103479 | 9 | AC004557 | AC004557 | Genomic s |
| C 105 | 20 | 3.2 | 761 | 3 | MID165RR | X84412 | D. labanonen | C 178 | 20 | 3.2 | 103479 | 9 | AC140059 | AC140059 | Homo sapi |
| C 106 | 20 | 3.2 | 761 | 3 | MID165RR | X84411 | D. nebulosa | C 179 | 20 | 3.2 | 109003 | 9 | AC006207 | AC006207 | Homo sapi |
| C 107 | 20 | 3.2 | 761 | 3 | ZAPMTRG16S | M93998 | Zapitonus t | C 180 | 20 | 3.2 | 109290 | 9 | AC108868 | AC108868 | Homo sapi |
| C 108 | 20 | 3.2 | 785 | 3 | DROMT165A | M93995 | Drosophila | C 181 | 20 | 3.2 | 110000 | 2 | AC091359_2 | AC091359_2 | Continuatio |
| C 109 | 20 | 3.2 | 799 | 3 | DROMT165B | M93996 | Drosophila | C 182 | 20 | 3.2 | 110000 | 2 | AC109667_2 | AC109667_2 | Continuatio |
| C 110 | 20 | 3.2 | 905 | 3 | DROMT165U | M93999 | Drosophila | C 183 | 20 | 3.2 | 110000 | 2 | AC000348 | AC000348 | Genomic s |
| C 111 | 20 | 3.2 | 905 | 3 | DROMT165V | M93997 | Drosophila | C 184 | 20 | 3.2 | 111566 | 8 | AC010445 | AC010445 | Homo sapi |
| C 112 | 20 | 3.2 | 905 | 3 | DROMT165X | M93992 | Drosophila | C 185 | 20 | 3.2 | 117072 | 9 | AL365440 | AL365440 | Human DNA |
| C 113 | 20 | 3.2 | 905 | 3 | DROMT165Y | M93993 | Drosophila | C 186 | 20 | 3.2 | 126954 | 9 | AC026917 | AC026917 | Homo sapi |
| C 114 | 20 | 3.2 | 905 | 3 | DROMT165Z | M93994 | Drosophila | C 187 | 20 | 3.2 | 127293 | 2 | AC073621 | AC073621 | Homo sapi |
| C 115 | 20 | 3.2 | 905 | 3 | DROMT165Z | M93988 | Drosophila | C 188 | 20 | 3.2 | 141048 | 9 | AC102307 | AC102307 | Mus muscu |
| C 116 | 20 | 3.2 | 905 | 3 | S45470 | S45470 | fragment b | C 189 | 20 | 3.2 | 142690 | 2 | AC102307 | AC102307 | Mus muscu |
| C 117 | 20 | 3.2 | 905 | 3 | S45471 | S45471 | fragment b | C 190 | 20 | 3.2 | 145697 | 9 | AC020642 | AC020642 | Homo sapi |
| C 118 | 20 | 3.2 | 905 | 3 | S45472 | S45472 | fragment b | C 191 | 20 | 3.2 | 146437 | 2 | AC0022836 | AC0022836 | Homo sapi |
| C 119 | 20 | 3.2 | 905 | 3 | S45475 | S45475 | fragment b | C 192 | 20 | 3.2 | 147118 | 9 | AC007513 | AC007513 | Homo sapi |
| C 120 | 20 | 3.2 | 1701 | 3 | AF164579 | AF164579 | Drosophila | C 193 | 20 | 3.2 | 150214 | 9 | AC011291 | AC011291 | Homo sapi |
| C 121 | 20 | 3.2 | 1702 | 3 | AF164578 | AF164578 | Drosophila | C 194 | 20 | 3.2 | 151252 | 2 | AC138387 | AC138387 | Mus muscu |
| C 122 | 20 | 3.2 | 1704 | 3 | AF164594 | AF164594 | Drosophila | C 195 | 20 | 3.2 | 151948 | 2 | AC022775 | AC022775 | Homo sapi |
| C 123 | 20 | 3.2 | 1704 | 3 | AF164596 | AF164596 | Drosophila | C 196 | 20 | 3.2 | 154080 | 2 | AC024416 | AC024416 | Homo sapi |
| C 124 | 20 | 3.2 | 1705 | 3 | AF164588 | AF164588 | Drosophila | C 197 | 20 | 3.2 | 155867 | 9 | AC109455 | AC109455 | Homo sapi |
| C 125 | 20 | 3.2 | 1705 | 3 | AF164589 | AF164589 | Drosophila | C 198 | 20 | 3.2 | 159791 | 9 | AC0007179 | AC0007179 | Homo sapi |
| C 126 | 20 | 3.2 | 1706 | 3 | AF164587 | AF164587 | Drosophila | C 199 | 20 | 3.2 | 163189 | 9 | AB045359 | AB045359 | Homo sapi |
| C 127 | 20 | 3.2 | 1710 | 3 | AF164581 | AF164581 | Drosophila | C 200 | 20 | 3.2 | 162549 | 9 | AC090802 | AC090802 | Homo sapi |
| C 128 | 20 | 3.2 | 1713 | 3 | AF164591 | AF164591 | Drosophila | C 201 | 20 | 3.2 | 162922 | 2 | AC011281 | AC011281 | Homo sapi |
| C 129 | 20 | 3.2 | 1713 | 3 | AF164592 | AF164592 | Drosophila | C 202 | 20 | 3.2 | 163634 | 2 | AC141374 | AC141374 | Rattus no |
| C 130 | 20 | 3.2 | 1713 | 3 | AF164593 | AF164593 | Drosophila | C 203 | 20 | 3.2 | 164636 | 2 | AC117783 | AC117783 | Mus muscu |
| C 131 | 20 | 3.2 | 1715 | 3 | AF164586 | AF164586 | Drosophila | C 204 | 20 | 3.2 | 166810 | 2 | AL590222 | AL590222 | Human DNA |
| C 132 | 20 | 3.2 | 1716 | 3 | AF164585 | AF164585 | Drosophila | C 205 | 20 | 3.2 | 167043 | 2 | AC111075 | AC111075 | Mus muscu |
| C 133 | 20 | 3.2 | 1717 | 3 | AF164583 | AF164583 | Drosophila | C 206 | 20 | 3.2 | 167166 | 2 | AC024654 | AC024654 | Homo sapi |
| C 134 | 20 | 3.2 | 1717 | 3 | AF164584 | AF164584 | Drosophila | C 207 | 20 | 3.2 | 167767 | 2 | AC102831 | AC102831 | Mus muscu |
| C 135 | 20 | 3.2 | 17365 | 1 | AE006083 | AE006083 | Pasteurel | C 208 | 20 | 3.2 | 168665 | 2 | AC053491 | AC053491 | Homo sapi |
| C 136 | 20 | 3.2 | 14365 | 1 | AE006097 | AE006097 | Drosophila | C 209 | 20 | 3.2 | 169246 | 2 | AC135840 | AC135840 | Sus scrofi |
| C 137 | 20 | 3.2 | 14365 | 1 | DME400907 | DME400907 | Drosophila | C 210 | 20 | 3.2 | 171561 | 2 | EX005081 | EX005081 | Danio rer |
| C 138 | 20 | 3.2 | 14905 | 3 | AF200828 | AF200828 | Drosophila | C 211 | 20 | 3.2 | 175551 | 2 | AC102866 | AC102866 | Mus muscu |

| | | | | | | | | | | | | | | |
|-------|----|-----|----------|----|----------|-----------|-----|----|-----|-------|----|-----------|-----------|--------------|
| C 212 | 20 | 3.2 | 172883 | 9 | AP003967 | Homo sapi | 285 | 19 | 3.1 | 1109 | 3 | PV1292977 | AJ2992977 | Plasmodi |
| C 213 | 20 | 3.2 | 174098 | 9 | AC005737 | Homo sapi | 286 | 19 | 3.1 | 1109 | 3 | PV1297403 | AJ297403 | Plasmodi |
| C 214 | 20 | 3.2 | 174316 | 9 | AC136975 | Mus muscu | 287 | 19 | 3.1 | 1113 | 3 | AF164605 | AF164605 | Plasmodi |
| C 215 | 20 | 3.2 | 178736 | 9 | AC103853 | Homo sapi | 288 | 19 | 3.1 | 1156 | 3 | PV008977 | U08977 | Plasmodi |
| C 216 | 20 | 3.2 | 180511 | 2 | AC139523 | Rattus no | 289 | 19 | 3.1 | 1161 | 3 | PFAC51X | L05066 | Plasmodi |
| C 217 | 20 | 3.2 | 182375 | 2 | AC105920 | Homo sapi | 290 | 19 | 3.1 | 1179 | 3 | PV1278611 | AJ278611 | Plasmodi |
| C 218 | 20 | 3.2 | 184989 | 2 | AC113352 | Homo sapi | 291 | 19 | 3.1 | 1179 | 3 | PV1400910 | AJ400910 | Plasmodi |
| C 219 | 20 | 3.2 | 185624 | 9 | AC103923 | Homo sapi | 292 | 19 | 3.1 | 1175 | 3 | PFAC5CA | M20670 | Plasmodi |
| C 220 | 20 | 3.2 | 187566 | 2 | AC139029 | Mus muscu | 293 | 19 | 3.1 | 1561 | 11 | AF383928 | AF383928 | Hevea brr |
| C 221 | 20 | 3.2 | 187727 | 2 | AC064806 | Homo sapi | 294 | 19 | 3.1 | 1711 | 3 | AF164582 | AF164582 | Drosophi |
| C 222 | 20 | 3.2 | 192296 | 2 | AC102197 | Mus muscu | 295 | 19 | 3.1 | 1793 | 3 | AF164580 | AF164580 | Drosophi |
| C 223 | 20 | 3.2 | 192626 | 2 | AC119958 | Mus muscu | 296 | 19 | 3.1 | 1895 | 3 | PFAC5A | M19526 | Plasmodi |
| C 224 | 20 | 3.2 | 193212 | 2 | AP004370 | Homo sapi | 297 | 19 | 3.1 | 1908 | 6 | 108489 | 108489 | Sequence |
| C 225 | 20 | 3.2 | 193390 | 2 | AC013730 | Homo sapi | 298 | 19 | 3.1 | 2211 | 9 | AC014697 | AC014697 | Drosophi |
| C 226 | 20 | 3.2 | 194331 | 2 | AC120280 | Rattus no | 299 | 19 | 3.1 | 4709 | 2 | HSB003323 | AL832016 | Homo sapi |
| C 227 | 20 | 3.2 | 196436 | 2 | BX511162 | Danio rer | 300 | 19 | 3.1 | 5849 | 3 | PBUT97311 | U79731 | Plasmodi |
| C 228 | 20 | 3.2 | 199230 | 2 | AC118531 | Rattus no | 301 | 19 | 3.1 | 10095 | 1 | AE011536 | AE011536 | Leptospir |
| C 229 | 20 | 3.2 | 200341 | 2 | AC138403 | Mus muscu | 302 | 19 | 3.1 | 10432 | 1 | AE014994 | AE014994 | Streptoco |
| C 230 | 20 | 3.2 | 203422 | 10 | AL713863 | Mus muscu | 303 | 19 | 3.1 | 11165 | 1 | AE006505 | AE006505 | Streptoco |
| C 231 | 20 | 3.2 | 203846 | 2 | AC119431 | Mus muscu | 304 | 19 | 3.1 | 11665 | 1 | AE009988 | AE009988 | Streptoco |
| C 232 | 20 | 3.2 | 209942 | 10 | AL845291 | Mouse DNA | 305 | 19 | 3.1 | 15865 | 2 | MTCOCNMR | X56015 | C-tribidia o |
| C 233 | 20 | 3.2 | 219248 | 2 | AC132858 | Mus muscu | 306 | 19 | 3.1 | 20663 | 2 | AC014972 | AC014972 | Drosophi |
| C 234 | 20 | 3.2 | 223606 | 2 | AC013479 | Homo sapi | 307 | 19 | 3.1 | 33837 | 3 | CEP27C8 | CEP27C8 | Caenorhadi |
| C 235 | 20 | 3.2 | 224146 | 2 | AC135462 | Rattus no | 308 | 19 | 3.1 | 33873 | 3 | CEP27C8 | CEP27C8 | Caenorhadi |
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| C 237 | 20 | 3.2 | 225639 | 2 | AC108073 | Homo sapi | 310 | 19 | 3.1 | 36893 | 9 | AC138034 | AC138034 | Homo sapi |
| C 238 | 20 | 3.2 | 220841 | 9 | AC103437 | Rattus no | 311 | 19 | 3.1 | 37515 | 6 | AX458481 | AX458481 | Sequence |
| C 239 | 20 | 3.2 | 232344 | 2 | AC111782 | Rattus no | 312 | 19 | 3.1 | 37640 | 9 | AC005605 | AC005605 | Homo sapi |
| C 240 | 20 | 3.2 | 232930 | 10 | AC113761 | Rattus no | 313 | 19 | 3.1 | 38413 | 9 | AC005601 | AC005601 | Homo sapi |
| C 241 | 20 | 3.2 | 240231 | 2 | AC129735 | Rattus no | 314 | 19 | 3.1 | 38952 | 3 | CEAC3 | AC005601 | Homo sapi |
| C 242 | 20 | 3.2 | 241883</ | | | | | | | | | | | |

| | | | | | | | | | | | |
|-------|----|------------|---|-----------|---------------------|-----|----|------------|----|-----------|----------------------|
| C 358 | 19 | 3.1 121664 | 9 | AC114498 | AC114498 Homo sapi | 431 | 19 | 3.1 171075 | 2 | AC026842 | AC026842 Homo sapi |
| C 359 | 19 | 3.1 122315 | 2 | AL389917 | AL389917 Homo sapi | 432 | 19 | 3.1 171972 | 2 | AC012388 | AC012388 Drosophila |
| C 360 | 19 | 3.1 124120 | 2 | AL157824 | AL157824 Homo sapi | 433 | 19 | 3.1 172539 | 2 | EX247948 | EX247948 Drosophila |
| C 361 | 19 | 3.1 124167 | 9 | AP001874 | AP001874 Homo sapi | 434 | 19 | 3.1 172805 | 9 | AL360270 | AL360270 Homo sapi |
| C 362 | 19 | 3.1 125150 | 2 | AC005450 | AC005450 Drosophila | 435 | 19 | 3.1 173074 | 2 | AC009703 | AC009703 Homo sapi |
| C 363 | 19 | 3.1 125623 | 3 | AC115559 | AC115559 Drosophila | 436 | 19 | 3.1 173376 | 2 | AC129175 | AC129175 Mus muscu |
| C 364 | 19 | 3.1 127340 | 9 | AC115599 | AC115599 Drosophila | 437 | 19 | 3.1 173512 | 9 | AC142333 | AC142333 Pan trogl |
| C 365 | 19 | 3.1 132943 | 9 | AC112907 | AC112907 Homo sapi | 438 | 19 | 3.1 173952 | 2 | AC080087 | AC080087 Homo sapi |
| C 366 | 19 | 3.1 133309 | 9 | AL1355003 | AL1355003 Human DNA | 439 | 19 | 3.1 174012 | 5 | AL929503 | AL929503 Zebrafish |
| C 367 | 19 | 3.1 133402 | 9 | AL137843 | AL137843 Human DNA | 440 | 19 | 3.1 174023 | 9 | AC080089 | AC080089 Homo sapi |
| C 368 | 19 | 3.1 135055 | 2 | AC011873 | AC011873 Homo sapi | 441 | 19 | 3.1 174302 | 9 | AC090710 | AC090710 Homo sapi |
| C 369 | 19 | 3.1 138177 | 9 | AC013926 | AC013926 Human DNA | 442 | 19 | 3.1 174470 | 2 | AC021888 | AC021888 Homo sapi |
| C 370 | 19 | 3.1 138251 | 9 | AC004908 | AC004908 Homo sapi | 443 | 19 | 3.1 174543 | 2 | AC025190 | AC025190 Drosophila |
| C 371 | 19 | 3.1 141166 | 2 | AC015578 | AC015578 Homo sapi | 444 | 19 | 3.1 174997 | 3 | AC008256 | AC008256 Drosophila |
| C 372 | 19 | 3.1 142157 | 2 | AC102412 | AC102412 Mus muscu | 445 | 19 | 3.1 175561 | 10 | AC124381 | AC124381 Mus muscu |
| C 373 | 19 | 3.1 144848 | 2 | AC140069 | AC140069 Mus muscu | 446 | 19 | 3.1 176312 | 2 | AC102442 | AC102442 Mus muscu |
| C 374 | 19 | 3.1 145055 | 3 | AC007453 | AC007453 Drosophila | 447 | 19 | 3.1 176595 | 3 | AC018483 | AC018483 Drosophila |
| C 375 | 19 | 3.1 145327 | 9 | AP004285 | AP004285 Homo sapi | 448 | 19 | 3.1 176982 | 5 | AL732610 | AL732610 Zebrafish |
| C 376 | 19 | 3.1 146585 | 8 | CNS0808 | CNS0808 Homo sapi | 449 | 19 | 3.1 177214 | 2 | AC119972 | AC119972 Mus muscu |
| C 377 | 19 | 3.1 146808 | 9 | AC097451 | AC097451 Homo sapi | 450 | 19 | 3.1 177717 | 9 | AC061958 | AC061958 Homo sapi |
| C 378 | 19 | 3.1 148257 | 2 | AC105992 | AC105992 Mus muscu | 451 | 19 | 3.1 177785 | 10 | AC126936 | AC126936 Mus muscu |
| C 379 | 19 | 3.1 148565 | 2 | AC022052 | AC022052 Homo sapi | 452 | 19 | 3.1 177991 | 2 | EX11030 | EX11030 Drosophila |
| C 380 | 19 | 3.1 149988 | 2 | AC011929 | AC011929 Homo sapi | 453 | 19 | 3.1 178501 | 2 | AL392165 | AL392165 Homo sapi |
| C 381 | 19 | 3.1 150109 | 2 | AC144706 | AC144706 Drosophila | 454 | 19 | 3.1 178501 | 2 | AC032027 | AC032027 Homo sapi |
| C 382 | 19 | 3.1 150497 | 2 | AC011860 | AC011860 Homo sapi | 455 | 19 | 3.1 179262 | 9 | AL355343 | AL355343 Homo sapi |
| C 383 | 19 | 3.1 150642 | 9 | AP016309 | AP016309 Homo sapi | 456 | 19 | 3.1 180423 | 9 | AC011475 | AC011475 Homo sapi |
| C 384 | 19 | 3.1 151079 | 9 | AP001596 | AP001596 Homo sapi | 457 | 19 | 3.1 180827 | 2 | EX284110 | EX284110 Drosophila |
| C 385 | 19 | 3.1 151846 | 2 | AC102315 | AC102315 Mus muscu | 458 | 19 | 3.1 181240 | 2 | AC140725 | AC140725 Homo sapi |
| C 386 | 19 | 3.1 152055 | 2 | AC118645 | AC118645 Mus muscu | 459 | 19 | 3.1 181266 | 2 | AC016131 | AC016131 Drosophila |
| C 387 | 19 | 3.1 152747 | 9 | AC068050 | AC068050 Homo sapi | 460 | 19 | 3.1 181935 | 2 | AC013387 | AC013387 Homo sapi |
| C 388 | 19 | 3.1 152892 | 9 | AC110274 | AC110274 Homo sapi | 461 | 19 | 3.1 182106 | 3 | AC091499 | AC091499 Drosophila |
| C 389 | 19 | 3.1 153649 | 9 | AL732372 | AL732372 Homo sapi | 462 | 19 | 3.1 182260 | 2 | AC112922 | AC112922 Mus muscu |
| C 390 | 19 | 3.1 153749 | 8 | AP003019 | AP003019 Homo sapi | 463 | 19 | 3.1 183496 | 2 | AC125075 | AC125075 Mus muscu |
| C 391 | 19 | 3.1 154065 | 2 | AC084079 | AC084079 Homo sapi | 464 | 19 | 3.1 183687 | 9 | AC064864 | AC064864 Homo sapi |
| C 392 | 19 | 3.1 154539 | 2 | AC079187 | AC079187 Homo sapi | 465 | 19 | 3.1 183794 | 2 | AC011877 | AC011877 Homo sapi |
| C 393 | 19 | 3.1 154695 | 2 | EX111160 | EX111160 Drosophila | 466 | 19 | 3.1 184040 | 2 | AC013327 | AC013327 Homo sapi |
| C 394 | 19 | 3.1 154848 | 9 | AC016555 | AC016555 Homo sapi | 467 | 19 | 3.1 184778 | 2 | AC023567 | AC023567 Homo sapi |
| C 395 | 19 | 3.1 155612 | 2 | AC127461 | AC127461 Drosophila | 468 | 19 | 3.1 185317 | 2 | AL159883 | AL159883 Homo sapi |
| C 396 | 19 | 3.1 156236 | 2 | AC135668 | AC135668 Rattus no | 469 | 19 | 3.1 185784 | 2 | AP006248 | AP006248 Mus muscu |
| C 397 | 19 | 3.1 156319 | 2 | AC102038 | AC102038 Mus muscu | 470 | 19 | 3.1 186457 | 9 | AC068359 | AC068359 Homo sapi |
| C 398 | 19 | 3.1 156909 | 9 | AB020863 | AB020863 Homo sapi | 471 | 19 | 3.1 186457 | 2 | AL391727 | AL391727 Homo sapi |
| C 399 | 19 | 3.1 157058 | 2 | CNS0578Y | CNS0578Y Homo sapi | 472 | 19 | 3.1 186457 | 2 | AC022990 | AC022990 Homo sapi |
| C 400 | 19 | 3.1 157292 | 2 | AC018966 | AC018966 Homo sapi | 473 | 19 | 3.1 187854 | 2 | AL159883 | AL159883 Homo sapi |
| C 401 | 19 | 3.1 158024 | 9 | AL603902 | AL603902 Homo sapi | 474 | 19 | 3.1 188218 | 2 | AP006248 | AP006248 Mus muscu |
| C 402 | 19 | 3.1 158745 | 9 | AL136456 | AL136456 Human DNA | 475 | 19 | 3.1 188218 | 2 | AL391727 | AL391727 Homo sapi |
| C 403 | 19 | 3.1 159596 | 9 | AC093289 | AC093289 Homo sapi | 476 | 19 | 3.1 189354 | 2 | AC022990 | AC022990 Homo sapi |
| C 404 | 19 | 3.1 160677 | 2 | AC125266 | AC125266 Mus muscu | 477 | 19 | 3.1 189354 | 2 | AL844883 | AL844883 Zebrafish |
| C 405 | 19 | 3.1 161238 | 9 | AP003127 | AP003127 Homo sapi | 478 | 19 | 3.1 189354 | 2 | PEU38804 | PEU38804 Porphyra pu |
| C 406 | 19 | 3.1 161280 | 9 | AC093903 | AC093903 Homo sapi | 479 | 19 | 3.1 191028 | 8 | AC010897 | AC010897 Homo sapi |
| C 407 | 19 | 3.1 162215 | 9 | AC004886 | AC004886 Homo sapi | 480 | 19 | 3.1 191130 | 2 | AL935124 | AL935124 Mus muscu |
| C 408 | 19 | 3.1 163012 | 3 | AC008289 | AC008289 Drosophila | 481 | 19 | 3.1 191590 | 2 | AC022825 | AC022825 Homo sapi |
| C 409 | 19 | 3.1 163584 | 9 | AC008056 | AC008056 Homo sapi | 482 | 19 | 3.1 191772 | 10 | AL929511 | AL929511 Mouse DNA |
| C 410 | 19 | 3.1 163585 | 5 | EX000453 | EX000453 Zebrafish | 483 | 19 | 3.1 192178 | 3 | AC116920 | AC116920 Drosophila |
| C 411 | 19 | 3.1 163866 | 5 | AL929590 | AL929590 Zebrafish | 484 | 19 | 3.1 192178 | 3 | CNS01DWO | CNS01DWO Human chr |
| C 412 | 19 | 3.1 164035 | 3 | AC007888 | AC007888 Drosophila | 485 | 19 | 3.1 192404 | 2 | AC127099 | AC127099 Rattus no |
| C 413 | 19 | 3.1 164235 | 2 | AC115018 | AC115018 Homo sapi | 486 | 19 | 3.1 192927 | 9 | AC142355 | AC142355 Pan trogl |
| C 414 | 19 | 3.1 164668 | 2 | AC091925 | AC091925 Homo sapi | 487 | 19 | 3.1 193559 | 9 | CNS01RPH4 | CNS01RPH4 Human chr |
| C 415 | 19 | 3.1 164748 | 9 | AC012139 | AC012139 Homo sapi | 488 | 19 | 3.1 194175 | 10 | AC084071 | AC084071 Mus muscu |
| C 416 | 19 | 3.1 164909 | 2 | AC127621 | AC127621 Rattus no | 489 | 19 | 3.1 194390 | 2 | EX465217 | EX465217 Drosophila |
| C 417 | 19 | 3.1 164921 | 8 | AP022186 | AP022186 Cynididum | 490 | 19 | 3.1 194508 | 2 | AC096667 | AC096667 Homo sapi |
| C 418 | 19 | 3.1 164872 | 2 | AC101994 | AC101994 Mus muscu | 491 | 19 | 3.1 195282 | 2 | AC144659 | AC144659 Rattus no |
| C 419 | 19 | 3.1 165036 | 8 | AP004273 | AP004273 Oryza sat | 492 | 19 | 3.1 195282 | 2 | AC126088 | AC126088 Rattus no |
| C 420 | 19 | 3.1 165139 | 9 | HS436K10 | HS436K10 Human DNA | 493 | 19 | 3.1 195866 | 3 | AY003872 | AY003872 Plasmodu |
| C 421 | 19 | 3.1 165358 | 2 | AC111045 | AC111045 Mus muscu | 494 | 19 | 3.1 195866 | 3 | AC139154 | AC139154 Mus muscu |
| C 422 | 19 | 3.1 166670 | 2 | AC101997 | AC101997 Mus muscu | 495 | 19 | 3.1 195866 | 3 | AC139154 | AC139154 Mus muscu |
| C 423 | 19 | 3.1 166928 | 2 | AC055861 | AC055861 Homo sapi | 496 | 19 | 3.1 195866 | 3 | AC139154 | AC139154 Mus muscu |
| C 424 | 19 | 3.1 167049 | 2 | AC009444 | AC009444 Homo sapi | 497 | 19 | 3.1 195866 | 3 | AC139154 | AC139154 Mus muscu |
| C 425 | 19 | 3.1 168594 | 9 | AP003970 | AP003970 Homo sapi | 498 | 19 | 3.1 195866 | 3 | AC139154 | AC139154 Mus muscu |
| C 426 | 19 | 3.1 168871 | 2 | AC016117 | AC016117 Drosophila | 499 | 19 | 3.1 195866 | 3 | AC139154 | AC139154 Mus muscu |
| C 427 | 19 | 3.1 168949 | 2 | EX470069 | EX470069 Drosophila | 500 | 19 | 3.1 195866 | 3 | AC139154 | AC139154 Mus muscu |
| C 428 | 19 | 3.1 169903 | 2 | AC069164 | AC069164 Homo sapi | 501 | 19 | 3.1 195866 | 3 | AC139154 | AC139154 Mus muscu |
| C 429 | 19 | 3.1 170370 | 2 | EX469915 | EX469915 Drosophila | 502 | 19 | 3.1 195866 | 3 | AC139154 | AC139154 Mus muscu |
| C 430 | 19 | 3.1 171042 | 2 | AC120521 | AC120521 Cantis fam | 503 | 19 | 3.1 195866 | 3 | CNS01DSEI | CNS01DSEI Human chr |

| | | | | | | | | | | | |
|-------|----|------------|----|----------|---------------------|-------|----|------------|----|-----------|-----------------------|
| C 504 | 19 | 3.1 204068 | 2 | AC103395 | AC103395 Mus muscu | 577 | 19 | 3.1 264752 | 10 | AL669856 | AL669856 Mouse DNA |
| C 505 | 19 | 3.1 204343 | 2 | AL359496 | AL359496 Homo sapi | C 578 | 19 | 3.1 266035 | 2 | AC127791 | AC127791 Rattus no |
| C 506 | 19 | 3.1 204520 | 10 | AC129181 | AC129181 Mus muscu | C 579 | 19 | 3.1 266391 | 2 | AC097092 | AC097092 Rattus no |
| C 507 | 19 | 3.1 205084 | 10 | AC121859 | AC121859 Mus muscu | C 580 | 19 | 3.1 266806 | 2 | AC129387 | AC129387 Rattus no |
| C 508 | 19 | 3.1 206893 | 2 | AC115569 | AC115569 Rattus no | C 581 | 19 | 3.1 267899 | 2 | AC096980 | AC096980 Rattus no |
| C 509 | 19 | 3.1 207129 | 2 | AC102377 | AC102377 Mus muscu | C 582 | 19 | 3.1 268213 | 2 | AC103285 | AC103285 Rattus no |
| C 510 | 19 | 3.1 207582 | 2 | AC144674 | AC144674 Rattus no | C 583 | 19 | 3.1 270068 | 2 | AC113213 | AC113213 Rattus no |
| C 511 | 19 | 3.1 208531 | 2 | AC132353 | AC132353 Mus muscu | C 584 | 19 | 3.1 275192 | 2 | AC119208 | AC119208 Rattus no |
| C 512 | 19 | 3.1 209280 | 2 | AC131427 | AC131427 Rattus no | C 585 | 19 | 3.1 280977 | 2 | AC129751 | AC129751 Rattus no |
| C 513 | 19 | 3.1 209521 | 9 | AC021649 | AC021649 Homo sapi | C 586 | 19 | 3.1 285045 | 2 | AC116217 | AC116217 Rattus no |
| C 514 | 19 | 3.1 210176 | 2 | AC102529 | AC102529 Mus muscu | C 587 | 19 | 3.1 294169 | 3 | AE003821 | AE003821 Drosophill |
| C 515 | 19 | 3.1 210385 | 2 | AC009627 | AC009627 Homo sapi | C 588 | 19 | 3.1 303808 | 3 | AE003452 | AE003452 Drosophill |
| C 516 | 19 | 3.1 210775 | 2 | AL732518 | AL732518 Mus muscu | C 589 | 19 | 3.1 309145 | 2 | AC105907 | AC105907 Mus muscu |
| C 517 | 19 | 3.1 211633 | 2 | AC073609 | AC073609 Mus muscu | C 590 | 19 | 3.1 312694 | 2 | AC105837 | AC105837 Rattus no |
| C 518 | 19 | 3.1 212416 | 2 | BX005288 | BX005288 Dantio rer | C 591 | 19 | 3.1 313050 | 3 | PPA929352 | PPA929352 Plasmodiu |
| C 519 | 19 | 3.1 213535 | 6 | AX197417 | AX197417 Sequence | C 592 | 19 | 3.1 325650 | 1 | AP005145 | AP005145 Streptoco |
| C 520 | 19 | 3.1 215335 | 6 | AX223856 | AX223856 Sequence | C 593 | 19 | 3.1 328900 | 1 | AP005279 | AP005279 Corynebact |
| C 521 | 19 | 3.1 216325 | 2 | AC120950 | AC120950 Rattus no | C 594 | 19 | 3.1 340000 | 9 | AP001696 | AP001696 Homo sapi |
| C 522 | 19 | 3.1 216719 | 2 | AC122363 | AC122363 Mus muscu | C 595 | 19 | 3.1 349751 | 3 | PFMAL4P3 | PFMAL4P3 Plasmodiu |
| C 523 | 19 | 3.1 217731 | 2 | AC136554 | AC136554 Rattus no | C 596 | 19 | 3.1 349960 | 6 | AX282125 | AX282125 Sequence |
| C 524 | 19 | 3.1 217015 | 3 | AE003788 | AE003788 Drosophill | C 597 | 19 | 3.1 349960 | 6 | AX282717 | AX282717 Sequence |
| C 525 | 19 | 3.1 217046 | 10 | AC122389 | AC122389 Mus muscu | C 598 | 19 | 3.1 349980 | 6 | AX127148 | AX127148 Sequence |
| C 526 | 19 | 3.1 217135 | 2 | AC134535 | AC134535 Mus muscu | C 599 | 19 | 3.1 349980 | 6 | AX127149 | AX127149 Sequence |
| C 527 | 19 | 3.1 218635 | 2 | AC118338 | AC118338 Rattus no | C 600 | 19 | 3.1 349980 | 6 | AX344559 | AX344559 Sequence |
| C 528 | 19 | 3.1 219711 | 2 | AC127995 | AC127995 Rattus no | C 601 | 19 | 3.1 349980 | 6 | AX573240 | AX573240 Sequence |
| C 529 | 19 | 3.1 219925 | 2 | AC113968 | AC113968 Mus muscu | C 602 | 18 | 2.9 349980 | 6 | AR290578 | AR290578 Sequence |
| C 530 | 19 | 3.1 220638 | 10 | AL645723 | AL645723 Mouse DNA | C 603 | 18 | 2.9 69 | 6 | AE26071 | AE26071 Sequence |
| C 531 | 19 | 3.1 223792 | 2 | AC134359 | AC134359 Rattus no | C 604 | 18 | 2.9 73 | 6 | 166509 | 166509 Sequence |
| C 532 | 19 | 3.1 223326 | 2 | AC127905 | AC127905 Rattus no | C 605 | 18 | 2.9 73 | 6 | 166518 | 166518 Sequence |
| C 533 | 19 | 3.1 224469 | 2 | AC107245 | AC107245 Rattus no | C 606 | 18 | 2.9 81 | 6 | 166524 | 166524 Sequence |
| C 534 | 19 | 3.1 226432 | 2 | AC134654 | AC134654 Rattus no | C 607 | 18 | 2.9 87 | 6 | A26058 | A26058 PI promoter |
| C 535 | 19 | 3.1 227550 | 2 | AC102686 | AC102686 Mus muscu | C 608 | 18 | 2.9 90 | 6 | A26059 | A26059 sPI promoter |
| C 536 | 19 | 3.1 228283 | 10 | AF312994 | AF312994 Mus muscu | C 609 | 18 | 2.9 90 | 6 | 166525 | 166525 Sequence |
| C 537 | 19 | 3.1 228326 | 2 | AC103363 | AC103363 Mus muscu | C 610 | 18 | 2.9 93 | 6 | A26057 | A26057 PI promoter |
| C 538 | 19 | 3.1 228989 | 2 | AC136274 | AC136274 Rattus no | C 611 | 18 | 2.9 93 | 6 | 166523 | 166523 Sequence |
| C 539 | 19 | 3.1 230754 | 5 | BX004888 | BX004888 Zebrafish | C 612 | 18 | 2.9 104 | 6 | A09227 | A09227 Synthetic n |
| C 540 | 19 | 3.1 233417 | 10 | AL844146 | AL844146 Mouse DNA | C 613 | 18 | 2.9 105 | 6 | A09226 | A09226 Synthetic n |
| C 541 | 19 | 3.1 234979 | 2 | AC139651 | AC139651 Rattus no | C 614 | 18 | 2.9 105 | 6 | E01046 | E01046 DNA sequenc |
| C 542 | 19 | 3.1 235426 | 2 | AC121074 | AC121074 Canis fam | C 615 | 18 | 2.9 108 | 6 | A09229 | A09229 Synthetic n |
| C 543 | 19 | 3.1 235553 | 2 | AC020742 | AC020742 Homo sapi | C 616 | 18 | 2.9 109 | 6 | A09228 | A09228 Synthetic n |
| C 544 | 19 | 3.1 236984 | 2 | BX470098 | BX470098 Dantio rer | C 617 | 18 | 2.9 142 | 6 | A26063 | A26063 annealed nu |
| C 545 | 19 | 3.1 237065 | 2 | AC128999 | AC128999 Rattus no | C 618 | 18 | 2.9 145 | 6 | HSAA11975 | HSAA11975 Homo sapi |
| C 546 | 19 | 3.1 237426 | 2 | AC095707 | AC095707 Rattus no | C 619 | 18 | 2.9 262 | 8 | AF119070 | AF119070 Saccharom |
| C 547 | 19 | 3.1 237712 | 9 | AC012634 | AC012634 Homo sapi | C 620 | 18 | 2.9 307 | 10 | MMDECORIN | MMDECORIN M.musculus |
| C 548 | 19 | 3.1 238158 | 2 | AC139244 | AC139244 Mus muscu | C 621 | 18 | 2.9 540 | 10 | AF054142 | AF054142 Rattus no |
| C 549 | 19 | 3.1 238818 | 2 | AC103320 | AC103320 Rattus no | C 622 | 18 | 2.9 555 | 14 | VACCH9 | VACCH9 Vaccinia vi |
| C 550 | 19 | 3.1 239246 | 2 | AC112938 | AC112938 Mus muscu | C 623 | 18 | 2.9 601 | 14 | VACIKPRA | VACIKPRA Vaccinia vi |
| C 551 | 19 | 3.1 239464 | 2 | AC103079 | AC103079 Rattus no | C 624 | 18 | 2.9 615 | 9 | HSAA12025 | HSAA12025 Homo sapi |
| C 552 | 19 | 3.1 243767 | 2 | AC111853 | AC111853 Rattus no | C 625 | 18 | 2.9 617 | 11 | G83731 | G83731 S209P6039RB |
| C 553 | 19 | 3.1 241393 | 2 | AC119105 | AC119105 Rattus no | C 626 | 18 | 2.9 639 | 9 | HSAA36341 | HSAA36341 Homo sapi |
| C 554 | 19 | 3.1 241396 | 2 | AC123333 | AC123333 Rattus no | C 627 | 18 | 2.9 645 | 11 | BV076336 | BV076336 S212P6820 |
| C 555 | 19 | 3.1 241725 | 2 | AC109724 | AC109724 Rattus no | C 628 | 18 | 2.9 650 | 1 | AY075119 | AY075119 Unculture |
| C 556 | 19 | 3.1 242598 | 2 | AC106081 | AC106081 Rattus no | C 629 | 18 | 2.9 687 | 3 | AF332475 | AF332475 Pulex sim |
| C 557 | 19 | 3.1 245273 | 2 | AC137407 | AC137407 Rattus no | C 630 | 18 | 2.9 687 | 3 | AF332476 | AF332476 Pulex sim |
| C 558 | 19 | 3.1 247037 | 2 | AC094028 | AC094028 Rattus no | C 631 | 18 | 2.9 711 | 3 | AF536641 | AF536641 Cryploceop |
| C 559 | 19 | 3.1 247730 | 2 | AC112120 | AC112120 Rattus no | C 632 | 18 | 2.9 805 | 9 | AF179694 | AF179694 Pongo pyg |
| C 560 | 19 | 3.1 248074 | 2 | AC097404 | AC097404 Rattus no | C 633 | 18 | 2.9 850 | 14 | VACCH9 | VACCH9 Vaccinia vac |
| C 561 | 19 | 3.1 249341 | 2 | AC111667 | AC111667 Rattus no | C 634 | 18 | 2.9 1029 | 10 | AF483502 | AF483502 Mus muscu |
| C 562 | 19 | 3.1 249984 | 2 | AC094845 | AC094845 Rattus no | C 635 | 18 | 2.9 1029 | 10 | AF483503 | AF483503 Mus muscu |
| C 563 | 19 | 3.1 252420 | 2 | AB014841 | AB014841 Plasmodiu | C 636 | 18 | 2.9 1041 | 9 | AY190752 | AY190752 Homo sapi |
| C 564 | 19 | 3.1 252902 | 2 | AC129164 | AC129164 Rattus no | C 637 | 18 | 2.9 1039 | 3 | AY135360 | AY135360 Plasmodiu |
| C 565 | 19 | 3.1 254007 | 2 | AC094413 | AC094413 Rattus no | C 638 | 18 | 2.9 1086 | 3 | AF163868 | AF163868 Ehirlichia |
| C 566 | 19 | 3.1 254573 | 2 | AC125554 | AC125554 Rattus no | C 639 | 18 | 2.9 1113 | 3 | AF164603 | AF164603 Plasmodiu |
| C 567 | 19 | 3.1 254646 | 2 | AC114850 | AC114850 Rattus no | C 640 | 18 | 2.9 1123 | 8 | AY168989 | AY168989 Arabidops |
| C 568 | 19 | 3.1 255448 | 2 | AC134596 | AC134596 Mus muscu | C 641 | 18 | 2.9 1182 | 3 | PFAPAENEG | PFAPAENEG Plasmodiu |
| C 569 | 19 | 3.1 257471 | 2 | AC114371 | AC114371 Rattus no | C 642 | 18 | 2.9 1182 | 3 | PSU09765 | PSU09765 Plasmodiu |
| C 570 | 19 | 3.1 257664 | 10 | AL627213 | AL627213 Mouse DNA | C 643 | 18 | 2.9 1182 | 3 | PVU09738 | PVU09738 Plasmodiu |
| C 571 | 19 | 3.1 259159 | 2 | AC113333 | AC113333 Rattus no | C 644 | 18 | 2.9 1189 | 1 | AF311966 | AF311966 Plasmodiu |
| C 572 | 19 | 3.1 260517 | 2 | AC111318 | AC111318 Rattus no | C 645 | 18 | 2.9 1212 | 3 | PPACSB | PPACSB Plasmodiu |
| C 573 | 19 | 3.1 260880 | 2 | AC134486 | AC134486 Rattus no | C 646 | 18 | 2.9 1212 | 3 | PPACSL | PPACSL Plasmodiu |
| C 574 | 19 | 3.1 262990 | 2 | AC096412 | AC096412 Rattus no | C 647 | 18 | 2.9 1272 | 3 | PPACSG | PPACSG Plasmodiu |
| C 575 | 19 | 3.1 263050 | 1 | AP000981 | AP000981 Sulfolobu | C 648 | 18 | 2.9 1281 | 3 | PPACSG | PPACSG Plasmodiu |
| C 576 | 19 | 3.1 263377 | 2 | AC105647 | AC105647 Rattus no | C 649 | 18 | 2.9 1311 | 10 | RRDECRNMR | RRDECRNMR R.rattus mR |

| | | | | | | | | | | | | | |
|-------|----|-----|-------|----|-----------|---------------------|-------|----|-----|-------|---|-----------|---------------------|
| 650 | 18 | 2.9 | 1335 | 3 | PFACSM | M15102 P.cynomolg1 | 723 | 18 | 2.9 | 16225 | 2 | AC015354 | AC015354 Drosophila |
| C 651 | 18 | 2.9 | 1372 | 10 | MPGII | X53929 M.musculus | C 724 | 18 | 2.9 | 17538 | 6 | AX346059 | AX346059 Sequence |
| C 652 | 18 | 2.9 | 1448 | 9 | AK025871 | AK025871 Homo sapi | 725 | 18 | 2.9 | 18047 | 9 | HSDMDALU | Y13186 Homo sapien |
| C 653 | 18 | 2.9 | 1479 | 10 | BC016419 | BC016419 Mus muscu | 726 | 18 | 2.9 | 18302 | 9 | AL450266 | AL450266 Human DNA |
| C 654 | 18 | 2.9 | 1547 | 10 | RNDCN | X59859 R.norvegicu | C 727 | 18 | 2.9 | 19295 | 2 | AC112177 | AC112177 Homo sapi |
| C 655 | 18 | 2.9 | 1605 | 10 | MUSMEL18 | D90085 Mus muscicu | C 728 | 18 | 2.9 | 19459 | 6 | AX344208 | AX344208 Homo sapi |
| C 656 | 18 | 2.9 | 1708 | 3 | AF164595 | AF164595 Drosophila | C 729 | 18 | 2.9 | 19459 | 6 | AX348959 | AX348959 Sequence |
| C 657 | 18 | 2.9 | 2000 | 6 | AX595024 | AX595024 Sequence | C 730 | 18 | 2.9 | 21509 | 3 | DMC25D2 | DMC25D2 Sequence |
| C 658 | 18 | 2.9 | 2000 | 6 | I08490 | I08490 Sequence 3 | C 731 | 18 | 2.9 | 24643 | 8 | SPAC6C3 | SPAC6C3 Sequence |
| C 660 | 18 | 2.9 | 2755 | 9 | AK074339 | AK074339 Homo sapi | C 732 | 18 | 2.9 | 25138 | 8 | HSTRER2 | HSTRER2 Homo sapi |
| C 661 | 18 | 2.9 | 2884 | 10 | BC031204 | BC031204 Mus muscu | C 733 | 18 | 2.9 | 25407 | 8 | AP006359 | AP006359 Homo sapi |
| C 662 | 18 | 2.9 | 2890 | 9 | BC041560 | BC041560 Homo sapi | C 734 | 18 | 2.9 | 26522 | 3 | U29537 | U29537 Sequence |
| C 663 | 18 | 2.9 | 2942 | 9 | AK094680 | AK094680 Homo sapi | C 735 | 18 | 2.9 | 27991 | 3 | CER44A6 | CER44A6 Sequence |
| C 664 | 18 | 2.9 | 3014 | 9 | HSU57317 | U57317 Homo sapien | C 736 | 18 | 2.9 | 29678 | 9 | HSDMDINT | HSDMDINT Sequence |
| C 665 | 18 | 2.9 | 3142 | 6 | AX704744 | AX704744 Sequence | C 737 | 18 | 2.9 | 32784 | 9 | CEP0865 | CEP0865 Sequence |
| C 666 | 18 | 2.9 | 3179 | 6 | AX003139 | AX003139 Sequence | C 738 | 18 | 2.9 | 33380 | 2 | AC139172 | AC139172 Homo sapi |
| C 667 | 18 | 2.9 | 3181 | 6 | AX338107 | AX338107 Sequence | C 739 | 18 | 2.9 | 33995 | 3 | CEK11B4 | CEK11B4 Sequence |
| C 668 | 18 | 2.9 | 3234 | 8 | NTA131837 | AJ131837 Nicotiana | C 740 | 18 | 2.9 | 35641 | 2 | AC014835 | AC014835 Homo sapi |
| C 669 | 18 | 2.9 | 3577 | 8 | SCYBR245C | Z36114 S.cerevisia | C 741 | 18 | 2.9 | 36885 | 3 | AC024881 | AC024881 Sequence |
| C 670 | 18 | 2.9 | 3846 | 1 | AY251553 | AY251553 Clostridi | C 742 | 18 | 2.9 | 37770 | 3 | AL355590 | AL355590 Homo sapi |
| C 671 | 18 | 2.9 | 4043 | 1 | CIOBN | D49340 Clostridium | C 743 | 18 | 2.9 | 39337 | 3 | U39848 | U39848 Sequence |
| C 672 | 18 | 2.9 | 4231 | 6 | AX210645 | AX210645 Sequence | C 744 | 18 | 2.9 | 39488 | 2 | DMC56F3 | DMC56F3 Sequence |
| C 673 | 18 | 2.9 | 4231 | 6 | AX686744 | AX686744 Sequence | C 745 | 18 | 2.9 | 39526 | 2 | AC003961 | AC003961 Homo sapi |
| C 674 | 18 | 2.9 | 4231 | 6 | AF071202 | AF071202 Homo sapi | C 746 | 18 | 2.9 | 39526 | 2 | AP001058 | AP001058 Homo sapi |
| C 675 | 18 | 2.9 | 4262 | 9 | BC027907 | BC027907 Homo sapi | C 747 | 18 | 2.9 | 41051 | 9 | AC144442 | AC144442 Homo sapi |
| C 676 | 18 | 2.9 | 4412 | 9 | AF169693 | AF169693 Homo sapi | C 748 | 18 | 2.9 | 41598 | 9 | HS16M16 | HS16M16 Sequence |
| C 677 | 18 | 2.9 | 4479 | 7 | CBCPHG1 | X53751 Clostridium | C 749 | 18 | 2.9 | 43129 | 2 | AC131379 | AC131379 Homo sapi |
| C 678 | 18 | 2.9 | 4592 | 7 | CSTC1TOX | D90210 Bacterioph | C 750 | 18 | 2.9 | 43553 | 2 | AL357372 | AL357372 Human DNA |
| C 679 | 18 | 2.9 | 4638 | 10 | BC032273 | BC032273 Mus muscu | C 751 | 18 | 2.9 | 43593 | 9 | AC003960 | AC003960 Homo sapi |
| C 680 | 18 | 2.9 | 4712 | 1 | CBPNC1M | X71126 C.potillium | C 752 | 18 | 2.9 | 43982 | 8 | AC007289 | AC007289 Homo sapi |
| C 681 | 18 | 2.9 | 5127 | 6 | AX344666 | AX344666 Sequence | C 753 | 18 | 2.9 | 44227 | 3 | AF275271 | AF275271 Sequence |
| C 682 | 18 | 2.9 | 5333 | 6 | AX598849 | AX598849 Sequence | C 754 | 18 | 2.9 | 45211 | 8 | U29381 | U29381 Sequence |
| C 683 | 18 | 2.9 | 5333 | 6 | AX598849 | AX598849 Sequence | C 755 | 18 | 2.9 | 45820 | 2 | AC014581 | AC014581 Homo sapi |
| C 684 | 18 | 2.9 | 5554 | 10 | AK122303 | AK122303 Mus muscu | C 756 | 18 | 2.9 | 46843 | 2 | SPBC530 | SPBC530 Sequence |
| C 685 | 18 | 2.9 | 5654 | 10 | MMU53155 | AJ53155 Mus muscu | C 757 | 18 | 2.9 | 50000 | 6 | AR211703 | AR211703 Sequence |
| C 686 | 18 | 2.9 | 5876 | 6 | AR261061 | AR261061 Sequence | C 758 | 18 | 2.9 | 50308 | 2 | AC099858 | AC099858 Mus muscu |
| C 687 | 18 | 2.9 | 6082 | 6 | AR278592 | AR278592 Sequence | C 759 | 18 | 2.9 | 50960 | 2 | AC017313 | AC017313 Homo sapi |
| C 688 | 18 | 2.9 | 6082 | 6 | AX141045 | AX141045 Sequence | C 760 | 18 | 2.9 | 51552 | 6 | AR266023 | AR266023 Sequence |
| C 689 | 18 | 2.9 | 6082 | 6 | AX200905 | AX200905 Sequence | C 761 | 18 | 2.9 | 51757 | 2 | AC007025 | AC007025 Homo sapi |
| C 690 | 18 | 2.9 | 6082 | 6 | AX267561 | AX267561 Sequence | C 762 | 18 | 2.9 | 53570 | 2 | AC100955 | AC100955 Homo sapi |
| C 691 | 18 | 2.9 | 6377 | 9 | HSW805107 | AL833850 Homo sapi | C 763 | 18 | 2.9 | 53932 | 2 | AC023371 | AC023371 Homo sapi |
| C 692 | 18 | 2.9 | 6533 | 14 | AF189155 | AF189155 Sequence | C 764 | 18 | 2.9 | 54472 | 8 | AP004542 | AP004542 Lotus jap |
| C 693 | 18 | 2.9 | 6550 | 14 | PVL50TKMO | Z65548 Puumala vir | C 765 | 18 | 2.9 | 54589 | 2 | AC014460 | AC014460 Drosophila |
| C 694 | 18 | 2.9 | 6710 | 6 | AX008265 | AX008265 Sequence | C 766 | 18 | 2.9 | 54727 | 2 | AL357336 | AL357336 Human DNA |
| C 695 | 18 | 2.9 | 7218 | 6 | I66494 | I66494 Sequence 14 | C 767 | 18 | 2.9 | 55161 | 2 | AC130684 | AC130684 Homo sapi |
| C 696 | 18 | 2.9 | 7285 | 8 | AF309806 | AF309806 Populus b | C 768 | 18 | 2.9 | 56531 | 2 | AC105232 | AC105232 Homo sapi |
| C 697 | 18 | 2.9 | 7379 | 8 | HSW803374 | AL832067 Homo sapi | C 769 | 18 | 2.9 | 56891 | 2 | AC101012 | AC101012 Mus muscu |
| C 698 | 18 | 2.9 | 7795 | 2 | AC066600 | AC066600 Homo sapi | C 770 | 18 | 2.9 | 57049 | 2 | HSW85A12 | HSW85A12 Sequence |
| C 699 | 18 | 2.9 | 7827 | 2 | AC017447 | AC017447 Drosophila | C 771 | 18 | 2.9 | 57893 | 2 | AC095868 | AC095868 Homo sapi |
| C 700 | 18 | 2.9 | 8313 | 6 | I66482 | I66482 Sequence 2 | C 772 | 18 | 2.9 | 58006 | 2 | AC005127 | AC005127 Sequence |
| C 701 | 18 | 2.9 | 8333 | 6 | AX277950 | AX277950 Sequence | C 773 | 18 | 2.9 | 58006 | 2 | AC002057 | AC002057 Drosophila |
| C 702 | 18 | 2.9 | 8333 | 6 | AX323641 | AX323641 Sequence | C 774 | 18 | 2.9 | 58460 | 9 | AL512299 | AL512299 Homo sapi |
| C 703 | 18 | 2.9 | 8333 | 6 | AX346404 | AX346404 Sequence | C 775 | 18 | 2.9 | 58473 | 9 | AL448103 | AL448103 Homo sapi |
| C 704 | 18 | 2.9 | 8710 | 6 | I60241 | I60241 Sequence 3 | C 776 | 18 | 2.9 | 58484 | 9 | AL137122 | AL137122 Human DNA |
| C 705 | 18 | 2.9 | 9019 | 6 | I60242 | I60242 Sequence 4 | C 777 | 18 | 2.9 | 59250 | 2 | AC144344 | AC144344 Human DNA |
| C 706 | 18 | 2.9 | 9064 | 8 | MTR417911 | MTR417911 Sequence | C 778 | 18 | 2.9 | 59272 | 2 | AL592490 | AL592490 Human DNA |
| C 707 | 18 | 2.9 | 9454 | 6 | I66483 | I66483 Sequence 3 | C 779 | 18 | 2.9 | 60391 | 3 | AC024796 | AC024796 Homo sapi |
| C 708 | 18 | 2.9 | 9613 | 1 | CBCCTOX | X62389 Botulinum b | C 780 | 18 | 2.9 | 60740 | 2 | AC016557 | AC016557 Sequence |
| C 709 | 18 | 2.9 | 9613 | 1 | CBCCTOX | X62389 Botulinum b | C 781 | 18 | 2.9 | 60778 | 2 | AC092921 | AC092921 Homo sapi |
| C 710 | 18 | 2.9 | 9689 | 1 | CBP1CWTCL | X64433 Clostridium | C 782 | 18 | 2.9 | 61392 | 2 | AC137565 | AC137565 Homo sapi |
| C 711 | 18 | 2.9 | 9917 | 6 | I66496 | I66496 Sequence 16 | C 783 | 18 | 2.9 | 61920 | 2 | AC021270 | AC021270 Homo sapi |
| C 712 | 18 | 2.9 | 10605 | 1 | AE015601 | AE015601 Shewanella | C 784 | 18 | 2.9 | 62909 | 6 | AX067457 | AX067457 Sequence |
| C 713 | 18 | 2.9 | 10781 | 9 | HSU58767 | U58767 Homo sapien | C 785 | 18 | 2.9 | 63571 | 3 | AC005126 | AC005126 Homo sapi |
| C 714 | 18 | 2.9 | 11505 | 1 | AE011693 | AE011693 Xanthomon | C 786 | 18 | 2.9 | 63931 | 2 | AC120211 | AC120211 Sequence |
| C 715 | 18 | 2.9 | 11614 | 1 | AB037166 | AB037166 Clostridi | C 787 | 18 | 2.9 | 64580 | 2 | AC106282 | AC106282 Homo sapi |
| C 716 | 18 | 2.9 | 11747 | 1 | AB061780 | AB061780 Clostridi | C 788 | 18 | 2.9 | 64840 | 2 | AC129551 | AC129551 Homo sapi |
| C 717 | 18 | 2.9 | 12297 | 7 | CBCBONT | X72793 Clostridium | C 789 | 18 | 2.9 | 66118 | 9 | AC109479 | AC109479 Homo sapi |
| C 718 | 18 | 2.9 | 12979 | 7 | AE012980 | AE012980 Thermococ | C 790 | 18 | 2.9 | 66898 | 2 | AC101234 | AC101234 Homo sapi |
| C 719 | 18 | 2.9 | 13326 | 14 | VACLVIPF | MS7977 Vaccinia vi | C 791 | 18 | 2.9 | 68790 | 9 | HSJ287H17 | HSJ287H17 Sequence |
| C 720 | 18 | 2.9 | 14867 | 3 | AE001398 | AE001398 Plasmodiu | C 792 | 18 | 2.9 | 68870 | 2 | AC130292 | AC130292 Homo sapi |
| C 721 | 18 | 2.9 | 16200 | 6 | AX405492 | AX405492 Sequence | C 793 | 18 | 2.9 | 68903 | 9 | HS92M18 | HS92M18 Sequence |
| C 722 | 18 | 2.9 | 16200 | 6 | AX405493 | AX405493 Sequence | C 795 | 18 | 2.9 | 70329 | 2 | AC087718 | AC087718 Homo sapi |

| | | | | | | | | | | | | | |
|-------|----|-----|--------|---|-----------|---------------------|-------|----|-----|--------|----|-----------|--------------------|
| C 796 | 18 | 2.9 | 71371 | 9 | AL356357 | Human DNA | C 869 | 18 | 2.9 | 106441 | 9 | HSJ803J11 | AL117350 Human DNA |
| C 797 | 18 | 2.9 | 72254 | 2 | AC019316 | AC019316 Homo sapi | C 870 | 18 | 2.9 | 107139 | 2 | AL360223 | AL360223 Homo sapi |
| C 798 | 18 | 2.9 | 72883 | 2 | AC023432 | AC023432 Homo sapi | C 871 | 18 | 2.9 | 107400 | 2 | AL141864 | AC141864 Homo sapi |
| C 799 | 18 | 2.9 | 73371 | 9 | AC004872 | AC004872 Homo sapi | C 872 | 18 | 2.9 | 107963 | 2 | AC144517 | AC144517 Homo sapi |
| C 800 | 18 | 2.9 | 73811 | 9 | AL355879 | AL355879 Human DNA | C 873 | 18 | 2.9 | 108718 | 2 | AC008837 | AC008837 Homo sapi |
| C 801 | 18 | 2.9 | 73881 | 9 | AC091817 | AC091817 Homo sapi | C 874 | 18 | 2.9 | 109224 | 2 | AL356434 | AL356434 Homo sapi |
| C 802 | 18 | 2.9 | 74237 | 9 | AC098809 | AC098809 Papio anu | C 875 | 18 | 2.9 | 109359 | 9 | AC004857 | AC004857 Homo sapi |
| C 803 | 18 | 2.9 | 74729 | 9 | HS703H14 | HS703H14 Homo sapi | C 876 | 18 | 2.9 | 109745 | 9 | AC025469 | AC025469 Homo sapi |
| C 804 | 18 | 2.9 | 75153 | 2 | AC134293 | AC134293 Rattus no | C 877 | 18 | 2.9 | 109891 | 9 | AL353897 | AL353897 Homo sapi |
| C 805 | 18 | 2.9 | 75276 | 2 | AC008861 | AC008861 Homo sapi | C 878 | 18 | 2.9 | 110000 | 2 | AC079625 | AC079625 Homo sapi |
| C 806 | 18 | 2.9 | 75359 | 9 | AL3590139 | AL3590139 Human DNA | C 879 | 18 | 2.9 | 110000 | 2 | AC079846 | AC079846 Homo sapi |
| C 807 | 18 | 2.9 | 76095 | 2 | AC012753 | AC012753 Drosophill | C 880 | 18 | 2.9 | 110000 | 2 | AC096395 | AC096395 Rattus no |
| C 808 | 18 | 2.9 | 76828 | 2 | AC032029 | AC032029 Homo sapi | C 881 | 18 | 2.9 | 110000 | 2 | AC117030 | AC117030 Homo sapi |
| C 809 | 18 | 2.9 | 77331 | 9 | AL354983 | AL354983 Human DNA | C 882 | 18 | 2.9 | 110000 | 2 | AC118144 | AC118144 Homo sapi |
| C 810 | 18 | 2.9 | 78467 | 9 | AC008078 | AC008078 Homo sapi | C 883 | 18 | 2.9 | 110000 | 2 | AC119122 | AC119122 Rattus no |
| C 811 | 18 | 2.9 | 79418 | 2 | AC005429 | AC005429 Drosophill | C 884 | 18 | 2.9 | 110000 | 2 | AC119122 | AC119122 Homo sapi |
| C 812 | 18 | 2.9 | 79480 | 2 | AC128461 | Continuation (5 of | C 885 | 18 | 2.9 | 110000 | 2 | AC128874 | AC128874 Rattus no |
| C 813 | 18 | 2.9 | 79506 | 9 | AL137247 | AL137247 Human DNA | C 886 | 18 | 2.9 | 110000 | 2 | AC127805 | AC127805 Homo sapi |
| C 814 | 18 | 2.9 | 81000 | 9 | AB038161 | AB038161 Homo sapi | C 887 | 18 | 2.9 | 110000 | 2 | AC127805 | AC127805 Homo sapi |
| C 815 | 18 | 2.9 | 81414 | 8 | AB024037 | AB024037 Arabidops | C 888 | 18 | 2.9 | 110000 | 2 | AC128296 | AC128296 Homo sapi |
| C 816 | 18 | 2.9 | 82483 | 9 | AL391058 | AL391058 Human DNA | C 889 | 18 | 2.9 | 110000 | 2 | AL731895 | AL731895 Homo sapi |
| C 817 | 18 | 2.9 | 83079 | 9 | AC004538 | AC004538 Homo sapi | C 890 | 18 | 2.9 | 110000 | 2 | BX324111 | BX324111 Homo sapi |
| C 818 | 18 | 2.9 | 83382 | 9 | AL390793 | AL390793 Human DNA | C 891 | 18 | 2.9 | 110000 | 2 | PFMAL13 | PFMAL13 Homo sapi |
| C 819 | 18 | 2.9 | 85638 | 9 | AC108126 | AC108126 Homo sapi | C 892 | 18 | 2.9 | 110000 | 2 | PFMAL6P1 | PFMAL6P1 Homo sapi |
| C 820 | 18 | 2.9 | 86162 | 2 | AC126786 | AC126786 Medicago | C 893 | 18 | 2.9 | 110000 | 2 | BD061520 | BD061520 Homo sapi |
| C 821 | 18 | 2.9 | 88512 | 8 | FL1H2 | FL1H2 Arabidops | C 894 | 18 | 2.9 | 110000 | 6 | AC145127 | AC145127 Homo sapi |
| C 822 | 18 | 2.9 | 88557 | 2 | AL136314 | AL136314 Human DNA | C 895 | 18 | 2.9 | 110000 | 8 | AF438325 | AF438325 Homo sapi |
| C 823 | 18 | 2.9 | 88735 | 2 | AF165178 | AF165178 Homo sapi | C 896 | 18 | 2.9 | 110000 | 9 | AF058825 | AF058825 Arabidops |
| C 824 | 18 | 2.9 | 90140 | 2 | AC021612 | AC021612 Homo sapi | C 897 | 18 | 2.9 | 110157 | 8 | AL354766 | AL354766 Homo sapi |
| C 825 | 18 | 2.9 | 90140 | 2 | AC021612 | AC021612 Homo sapi | C 898 | 18 | 2.9 | 110575 | 2 | AL354766 | AL354766 Homo sapi |
| C 826 | 18 | 2.9 | 90441 | 2 | AC123574 | AC123574 Medicago | C 899 | 18 | 2.9 | 110752 | 8 | AP004969 | AP004969 Lotus jap |
| C 827 | 18 | 2.9 | 90461 | 2 | AC118467 | Continuation (5 of | C 900 | 18 | 2.9 | 111170 | 8 | AL354766 | AL354766 Homo sapi |
| C 828 | 18 | 2.9 | 90604 | 9 | AC006525 | AC006525 Homo sapi | C 901 | 18 | 2.9 | 111491 | 8 | HSJ617C6 | HSJ617C6 Homo sapi |
| C 829 | 18 | 2.9 | 90737 | 9 | AP001351 | AP001351 Homo sapi | C 902 | 18 | 2.9 | 111517 | 8 | ATF11C18 | ATF11C18 Homo sapi |
| C 830 | 18 | 2.9 | 91172 | 9 | AL356601 | AL356601 Human DNA | C 903 | 18 | 2.9 | 112672 | 9 | AC010455 | AC010455 Homo sapi |
| C 831 | 18 | 2.9 | 91228 | 8 | ATF14M19 | ATF14M19 Arabidops | C 904 | 18 | 2.9 | 112846 | 2 | AP000718 | AP000718 Homo sapi |
| C 832 | 18 | 2.9 | 91469 | 9 | AL356963 | AL356963 Human DNA | C 905 | 18 | 2.9 | 112846 | 2 | AL356963 | AL356963 Homo sapi |
| C 833 | 18 | 2.9 | 91987 | 9 | AC125362 | AC125362 Homo sapi | C 906 | 18 | 2.9 | 113329 | 9 | AL356963 | AL356963 Homo sapi |
| C 834 | 18 | 2.9 | 92376 | 8 | AC006282 | AC006282 Arabidops | C 907 | 18 | 2.9 | 113729 | 9 | AF260011 | AF260011 Homo sapi |
| C 835 | 18 | 2.9 | 92493 | 8 | ATTT2317 | ATTT2317 Arabidops | C 908 | 18 | 2.9 | 113826 | 9 | AL133378 | AL133378 Human DNA |
| C 836 | 18 | 2.9 | 92564 | 9 | ATY007685 | ATY007685 Homo sapi | C 909 | 18 | 2.9 | 114022 | 9 | AL157952 | AL157952 Homo sapi |
| C 837 | 18 | 2.9 | 92883 | 2 | AC142027 | AC142027 Rattus no | C 910 | 18 | 2.9 | 115304 | 9 | AL138775 | AL138775 Human DNA |
| C 838 | 18 | 2.9 | 93609 | 2 | AL357673 | AL357673 Homo sapi | C 911 | 18 | 2.9 | 115767 | 2 | AC012310 | AC012310 Homo sapi |
| C 839 | 18 | 2.9 | 93717 | 9 | AL357673 | AL357673 Human DNA | C 912 | 18 | 2.9 | 116476 | 2 | AC127167 | AC127167 Homo sapi |
| C 840 | 18 | 2.9 | 94516 | 9 | AC112126 | AC112126 Homo sapi | C 913 | 18 | 2.9 | 116513 | 9 | HS48737 | HS48737 Homo sapi |
| C 841 | 18 | 2.9 | 94730 | 9 | AP0000230 | AP0000230 Homo sapi | C 914 | 18 | 2.9 | 116629 | 2 | AC111485 | AC111485 Homo sapi |
| C 842 | 18 | 2.9 | 95347 | 9 | HSJ081L22 | HSJ081L22 Homo sapi | C 915 | 18 | 2.9 | 116795 | 9 | AC015060 | AC015060 Homo sapi |
| C 843 | 18 | 2.9 | 96203 | 9 | AL135788 | AL135788 Human DNA | C 916 | 18 | 2.9 | 117585 | 8 | AC023279 | AC023279 Homo sapi |
| C 844 | 18 | 2.9 | 96285 | 8 | ATF10N7 | ATF10N7 Arabidops | C 917 | 18 | 2.9 | 117723 | 9 | AC116365 | AC116365 Homo sapi |
| C 845 | 18 | 2.9 | 96843 | 9 | AC009496 | AC009496 Homo sapi | C 918 | 18 | 2.9 | 117755 | 9 | AC092686 | AC092686 Homo sapi |
| C 846 | 18 | 2.9 | 97653 | 2 | AC137570 | AC137570 Homo sapi | C 919 | 18 | 2.9 | 117951 | 9 | AL359821 | AL359821 Human DNA |
| C 847 | 18 | 2.9 | 97736 | 9 | AC0093845 | AC0093845 Homo sapi | C 920 | 18 | 2.9 | 117954 | 9 | AC002065 | AC002065 Homo sapi |
| C 848 | 18 | 2.9 | 97818 | 2 | AC011859 | AC011859 Homo sapi | C 921 | 18 | 2.9 | 118335 | 8 | AC006193 | AC006193 Arabidops |
| C 849 | 18 | 2.9 | 98391 | 2 | AC106733 | AC106733 Homo sapi | C 922 | 18 | 2.9 | 118453 | 2 | AC135796 | AC135796 Homo sapi |
| C 850 | 18 | 2.9 | 98613 | 2 | AC013426 | AC013426 Homo sapi | C 923 | 18 | 2.9 | 118531 | 2 | AC020205 | AC020205 Homo sapi |
| C 851 | 18 | 2.9 | 99369 | 9 | AC112140 | AC112140 Homo sapi | C 924 | 18 | 2.9 | 118995 | 9 | AC005368 | AC005368 Homo sapi |
| C 852 | 18 | 2.9 | 99630 | 2 | AC142060 | AC142060 Rattus no | C 925 | 18 | 2.9 | 120638 | 2 | AC122168 | AC122168 Homo sapi |
| C 853 | 18 | 2.9 | 100000 | 2 | AP0000144 | AP0000144 Homo sapi | C 926 | 18 | 2.9 | 120962 | 2 | AC141114 | AC141114 Homo sapi |
| C 854 | 18 | 2.9 | 101244 | 2 | AC121334 | AC121334 Medicago | C 927 | 18 | 2.9 | 120985 | 2 | AC099651 | AC099651 Homo sapi |
| C 855 | 18 | 2.9 | 101363 | 9 | AC129090 | AC129090 Medicago | C 928 | 18 | 2.9 | 121129 | 9 | AL357315 | AL357315 Human DNA |
| C 856 | 18 | 2.9 | 101611 | 9 | AC018706 | AC018706 Homo sapi | C 929 | 18 | 2.9 | 122049 | 9 | HSB16C10 | HSB16C10 Homo sapi |
| C 857 | 18 | 2.9 | 103487 | 9 | AL449343 | AL449343 Human DNA | C 930 | 18 | 2.9 | 122107 | 2 | AC144482 | AC144482 Homo sapi |
| C 858 | 18 | 2.9 | 104008 | 2 | AC140022 | AC140022 Medicago | C 931 | 18 | 2.9 | 122135 | 2 | AC137552 | AC137552 Homo sapi |
| C 859 | 18 | 2.9 | 104339 | 2 | AP235105 | AP235105 Homo sapi | C 932 | 18 | 2.9 | 122665 | 2 | BX004777 | BX004777 Homo sapi |
| C 860 | 18 | 2.9 | 104573 | 2 | AC144618 | AC144618 Medicago | C 933 | 18 | 2.9 | 122986 | 2 | AC004915 | AC004915 Homo sapi |
| C 861 | 18 | 2.9 | 104687 | 2 | AC144724 | AC144724 Medicago | C 934 | 18 | 2.9 | 123147 | 2 | AC140029 | AC140029 Homo sapi |
| C 862 | 18 | 2.9 | 104738 | 8 | ATF20B18 | ATF20B18 Arabidops | C 935 | 18 | 2.9 | 123631 | 9 | HS22F01 | HS22F01 Homo sapi |
| C 863 | 18 | 2.9 | 104846 | 9 | HSB54J16 | HSB54J16 Human DNA | C 936 | 18 | 2.9 | 123829 | 10 | AC113263 | AC113263 Homo sapi |
| C 864 | 18 | 2.9 | 105335 | 9 | AC107374 | AC107374 Human DNA | C 937 | 18 | 2.9 | 125170 | 2 | AC133796 | AC133796 Homo sapi |
| C 865 | 18 | 2.9 | 105516 | 2 | AL512786 | AL512786 Homo sapi | C 938 | 18 | 2.9 | 125357 | 2 | AC136974 | AC136974 Homo sapi |
| C 866 | 18 | 2.9 | 105657 | 2 | AL365503 | AL365503 Human DNA | C 939 | 18 | 2.9 | 125403 | 9 | AC008929 | AC008929 Homo sapi |
| C 867 | 18 | 2.9 | 105857 | 2 | AC140028 | AC140028 Medicago | C 940 | 18 | 2.9 | 125720 | 2 | AC136138 | AC136138 Homo sapi |
| C 868 | 18 | 2.9 | 106180 | 2 | AC144728 | AC144728 Medicago | C 941 | 18 | 2.9 | 125992 | 2 | AC142222 | AC142222 Homo sapi |

| | | | | | | |
|------|----|-----|--------|----|----------|---------------------|
| 942 | 18 | 2.9 | 126469 | 9 | AC090022 | AC090022 Homo sapi |
| 943 | 18 | 2.9 | 126501 | 9 | HS708F5 | AL031782 Human DNA |
| 944 | 18 | 2.9 | 127757 | 9 | AC004468 | AC004468 Homo sapi |
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| 946 | 18 | 2.9 | 128386 | 2 | AC135678 | AL356782 Human DNA |
| 947 | 18 | 2.9 | 128595 | 2 | AL136179 | AL136179 Human DNA |
| 948 | 18 | 2.9 | 128728 | 8 | AC126794 | AC126794 Human DNA |
| 949 | 18 | 2.9 | 129512 | 8 | AL513221 | AL513221 Homo sapi |
| 950 | 18 | 2.9 | 130412 | 2 | AL669868 | AL669868 Mouse DNA |
| 951 | 18 | 2.9 | 131266 | 10 | AC122207 | AC122207 Mus muscu |
| 952 | 18 | 2.9 | 131490 | 3 | AC116330 | AC116330 Dictyoste |
| 953 | 18 | 2.9 | 132254 | 8 | AC126785 | AC126785 Medicago |
| 954 | 18 | 2.9 | 132702 | 8 | AC073510 | AC073510 Homo sapi |
| 955 | 18 | 2.9 | 133085 | 2 | AL512364 | AL512364 Homo sapi |
| 956 | 18 | 2.9 | 133226 | 2 | AC107079 | AC107079 Homo sapi |
| 957 | 18 | 2.9 | 133304 | 9 | AC096666 | AC096666 Homo sapi |
| 958 | 18 | 2.9 | 133847 | 2 | AC073383 | AC073383 Homo sapi |
| 959 | 18 | 2.9 | 134105 | 2 | AL444151 | AL444151 Mouse DNA |
| 960 | 18 | 2.9 | 134350 | 2 | AP004803 | AP004803 Oryza sat |
| 961 | 18 | 2.9 | 134513 | 10 | AC090440 | AC090440 Homo sapi |
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| 963 | 18 | 2.9 | 134628 | 9 | AC016689 | AC016689 Homo sapi |
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| 965 | 18 | 2.9 | 134841 | 9 | AC084873 | AC084873 Homo sapi |
| 966 | 18 | 2.9 | 135089 | 2 | AC005858 | AC005858 Homo sapi |
| 967 | 18 | 2.9 | 135298 | 2 | AL583854 | AL583854 Human DNA |
| 968 | 18 | 2.9 | 135521 | 9 | AC116724 | AC116724 Mus muscu |
| 969 | 18 | 2.9 | 135953 | 9 | BS111307 | BS111307 Dantio rer |
| 970 | 18 | 2.9 | 137125 | 2 | AC144592 | AC144592 Medicago |
| 971 | 18 | 2.9 | 137260 | 2 | AC025009 | AC025009 Homo sapi |
| 972 | 18 | 2.9 | 137820 | 2 | AC055854 | AC055854 Homo sapi |
| 973 | 18 | 2.9 | 137863 | 2 | AL137793 | AL137793 Human DNA |
| 974 | 18 | 2.9 | 137995 | 2 | AC020447 | AC020447 Drosophil |
| 975 | 18 | 2.9 | 138388 | 9 | AC127021 | AC127021 Medicago |
| 976 | 18 | 2.9 | 138419 | 2 | AC060794 | AC060794 Homo sapi |
| 977 | 18 | 2.9 | 138618 | 2 | AC136082 | AC136082 Rattus no |
| 978 | 18 | 2.9 | 138655 | 2 | HS142F18 | HS142F18 Human DNA |
| 979 | 18 | 2.9 | 139045 | 2 | AC119415 | AC119415 Medicago |
| 980 | 18 | 2.9 | 139287 | 2 | AC024118 | AC024118 Homo sapi |
| 981 | 18 | 2.9 | 139370 | 2 | AC016565 | AC016565 Homo sapi |
| 982 | 18 | 2.9 | 139444 | 9 | AC008961 | AC008961 Homo sapi |
| 983 | 18 | 2.9 | 139655 | 2 | BS11060 | BS11060 Dantio rer |
| 984 | 18 | 2.9 | 139788 | 2 | AC104465 | AC104465 Homo sapi |
| 985 | 18 | 2.9 | 140092 | 2 | AC046150 | AC046150 Mus muscu |
| 986 | 18 | 2.9 | 140200 | 2 | AL138828 | AL138828 Human DNA |
| 987 | 18 | 2.9 | 140201 | 2 | AC138465 | AC138465 Medicago |
| 988 | 18 | 2.9 | 140476 | 2 | AL031073 | AL031073 Human DNA |
| 989 | 18 | 2.9 | 140499 | 2 | AL928919 | AL928919 Mouse DNA |
| 990 | 18 | 2.9 | 141540 | 9 | AC092713 | AC092713 Homo sapi |
| 991 | 18 | 2.9 | 141582 | 2 | AC099817 | AC099817 Homo sapi |
| 992 | 18 | 2.9 | 141672 | 10 | AL929053 | AL929053 Zebrafish |
| 993 | 18 | 2.9 | 142087 | 2 | AC008749 | AC008749 Homo sapi |
| 994 | 18 | 2.9 | 142139 | 5 | AC136150 | AC136150 Oryza sat |
| 995 | 18 | 2.9 | 142345 | 5 | AC106793 | AC106793 Homo sapi |
| 996 | 18 | 2.9 | 142439 | 9 | AC003074 | AC003074 Homo sapi |
| 997 | 18 | 2.9 | 143439 | 9 | | |
| 998 | 18 | 2.9 | 143884 | 2 | | |
| 999 | 18 | 2.9 | 143887 | 2 | | |
| 1000 | 18 | 2.9 | 143878 | 9 | | |

ALIGNMENTS

RESULT 1
LOCUS G04707 254 bp DNA
DEFINITION human STS WI-4862, sequence tagged site.
ACCESSION G04707
VERSION G04707.1 GI:721665
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
TITLE Whitehead Institute/MIT Center for Genome Research; Random Genome
JOURNAL Unpublished (1995)
AUTHORS 2 (bases 1 to 254)
Hudson, T.
REFERENCE
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
JOURNAL Unpublished (1995)
COMMENT
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: AAAACATGTTTATTCCTCAGAGA
Primer B: TCTGGAATTTTGTCTAAACACA
STS size: 202
PCR Profile:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3.
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1..254
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="804_B_6; 946_D_3; 938_G_10; 951_H_12"
STS
primer_bind 51..252
primer_bind 51..74
BASE COUNT 105 a 34 c 35 g 79 t 1 others

FEATURES
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1..254
Location/Qualifiers
1..254
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/map="804_B_6; 946_D_3; 938_G_10; 951_H_12"

Query Match 3.5%; Score 22; DB 11; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OR 228 ATATGCTTATTATTATGTT 249
DB 205 ATATGCTTATTATTATGTT 226

RESULT 2
LOCUS HS12409 108534 bp DNA
DEFINITION Human DNA sequence from clone RPI-12409 on chromosome 6q21,
ACCESSION complete sequence.
VERSION AL021327
KEYWORDS AL021327.1 GI:2804157
SOURCE HMG.
ORGANISM Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 108534)
 AUTHORS Phillips, S
 TITLE Direct Submission
 JOURNAL Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 Clone requests: clonerequest@sanger.ac.uk
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk

 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>
 RP1-12409 is from the library RP1-1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pCYPAC2.

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 /clone_id="RP1-1"
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 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 228 ATATGCTTTATTTATTTATGTT 249
 ||||||||||||||||||||
 Db 16369 ATATGCTTTATTTATTTATGTT 16390
 ||||||||||||||||||||
 RESULT 3
 AC141496/c 127699 bp DNA linear HTG 24-MAR-2003
 LOCUS Rattus norvegicus clone CH230-511K8, WORKING DRAFT SEQUENCE, 8
 DEFINITION unorderd pieces.
 AC141496
 VERSION AC141496.2 GI:29165563
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 Rattus norvegicus (Norway rat)
 SOURCE

ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 127699)
 REFERENCE
 AUTHORS Muzny, D., Marle, M., Metker, M., Lee, A., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D., Anylebech, V., Aoyagi, A., Ayodeji, M., Bacc, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bismalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bunay, C., Burck, P., Butrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy, C., De Ande, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durkin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisl, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorj, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunarane, P., Haland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hughes, M., Hollins, B., Howells, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpachy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Loushewala, L., Louised, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmood, M., Malloy, K., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Mirza, E., Montemayor, U., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokelele, O., Okwom, G., Olarnunagsoon, A., Pal, S., Parks, K., Patel, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poldexter, A., Popovic, D., Primus, E., Pu, L., Pu, L., Quiroz, J., Rechlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sanders, W., Savery, G., Scherer, S., Scott, G., Shattman, S., Shen, H., Shetty, J., Shvartbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Speed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, D., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Woodden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.
 TITLE
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 127699)
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (17-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 127699)
 REFERENCE
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Mar 24, 2003 this sequence version replaced gi:28975757.

 COMMENT
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

```

----- Project Information
Center project name: KEGG
Center clone name: CH230-511K8
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 124484 bases at least Q40
Consensus quality: 125345 bases at least Q30
Consensus quality: 125900 bases at least Q20
Estimated insert size: 126226; sum-of-coverage estimation
Quality coverage: 5x in Q20 bases; sum-of-coverage estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1805: contig of 1805 bp in length
*
1806 1905: gap of unknown length
*
1906 4652: contig of 2747 bp in length
*
4653 4752: gap of unknown length
*
4753 8159: contig of 3407 bp in length
*
8160 8259: gap of unknown length
*
8260 13974: contig of 5715 bp in length
*
13975 14074: gap of unknown length
*
14075 22226: contig of 8152 bp in length
*
22227 22326: gap of unknown length
*
22327 41656: contig of 19330 bp in length
*
41657 41756: gap of unknown length
*
41757 78480: contig of 36724 bp in length
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78481 78580: gap of unknown length
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78581 127699: contig of 49119 bp in length.
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/db_xref="taxon:10116"
/clone="CH230-511K8"

BASE COUNT 40596 a 22414 c 23032 g 40955 t 702 others

ORIGIN
Query Match 3.5%; Score 22; DB 2; Length 127699;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 180 CTATATTTTACGATCATTT 201
Db 126250 CTATATTTTACGATCATTT 126229

RESULT 4
AL135926/c 158519 bp DNA linear PRI 30-NOV-2000
LOCUS Human DNA sequence from clone RP11-375F2 on chromosome 1 Contains a
DEFINITION pseudogene similar to Ubql (ubiquitin-like 1 (sentrin)), a
pseudogene similar to ribosomal protein L29, ESTs, STSs and GSSs,
complete sequence.
ACCESSION AL135926
VERSION AL135926.12 GI:9801286
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 158519)
AUTHORS Chapman,J.
TITLE Direct Submission

```

JOURNAL COMMENT

Submitted (03-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requesters: clonerequest@sanger.ac.uk

On Aug 14, 2000 this sequence version replaced gi:9621473. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human Chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>

RP11-375F2 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR:PBAC3.6>

IMPORTANT: This sequence is not the entire insert of clone RP11-375F2 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-375F2 is at 158519 in this sequence. The true right end of clone RP1-10C16 is at 100 in this sequence.

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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="RP11-375F2"
/chromosome="1"
/clone_11b="RPCI-11.2"
/clone_11b="RPCI-11.2"
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1465..1514
/note="25 copies 2 mer to 72% conserved"
1775..1824
/note="MIR repeat: matches 85..135 of consensus"
3415..3734
/note="L2 repeat: matches 2373..2707 of consensus"
4294..5519
/note="L1MB7 repeat: matches 4938..6173 of consensus"
5535..5640
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5652..5945
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5997..6055
/note="L1MB5 repeat: matches 5413..5471 of consensus"
6061..6158
/note="Alu repeat: matches 214..311 of consensus"
6160..6855
/note="L1MB5 repeat: matches 5460..6168 of consensus"
6919..7101
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7099..7228
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repeat_region      14045..14226
                    /note="MLTIE repeat: matches 385..567 of consensus"
misc_feature        complement(14529..15003)
                    /note="match: GSS: Em:AQ798857"
misc_feature        14901..15366
                    /note="match: GSS: Em:AQ221861"
repeat_region      15371..15463
                    /note="MIR repeat: matches 60..153 of consensus"
repeat_region      16536..16633
                    /note="L1MA repeat: matches 3093..3194 of consensus"
repeat_region      16839..17215
                    /note="L1PA7 repeat: matches 5767..6143 of consensus"
repeat_region      17225..17961
                    /note="L1PA3 repeat: matches 5410..6146 of consensus"
repeat_region      17962..19671
                    /note="L1PA7 repeat: matches 4077..5788 of consensus"
repeat_region      19672..20271
                    /note="L1PA7 repeat: matches 3477..4076 of consensus"
repeat_region      20277..20462
                    /note="L1MA repeat: matches 3403..3585 of consensus"
repeat_region      20479..21023
                    /note="L1PA8 repeat: matches -1540..-1003 of consensus"
repeat_region      21083..22136
                    /note="L1PA8 repeat: matches -977..1014 of consensus"
repeat_region      22104..24249
                    /note="L1M2 repeat: matches 37..2571 of consensus"
repeat_region      24175..24890
                    /note="L1 repeat: matches 2118..2843 of consensus"
repeat_region      24896..25532
                    /note="L1M1 repeat: matches 5508..6163 of consensus"
repeat_region      25865..25900
                    /note="6 copies 6 mer tGtGtG 97% conserved"
repeat_region      25903..26184
                    /note="AluY repeat: matches 1..282 of consensus"
misc_feature        27110..27647
                    /note="match: STS: Em:HS045M12S"
repeat_region      27233..27346
                    /note="L2 repeat: matches 2549..2668 of consensus"
repeat_region      27347..27437
                    /note="L2 repeat: matches 2664..2155 of consensus"
repeat_region      27438..27487
                    /note="L1M1 repeat: matches 5637..5685 of consensus"
repeat_region      27552..27933

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repeat_region      /note="L1MC4 repeat: matches 6621..7006 of consensus"
                    27982..28315
repeat_region      /note="L1MC4 repeat: matches 7094..7422 of consensus"
                    28256..28552
repeat_region      /note="L1MC5 repeat: matches 7262..7589 of consensus"
                    28629..28938
repeat_region      /note="AluY repeat: matches 1..310 of consensus"
                    29045..29218
repeat_region      /note="L1M1 repeat: matches 5338..5450 of consensus"
                    30188..30300
repeat_region      /note="MIR repeat: matches 71..190 of consensus"
                    30761..30877
repeat_region      /note="L2 repeat: matches 2362..2474 of consensus"
                    31253..31494
repeat_region      /note="L2 repeat: matches 466..712 of consensus"
                    31722..33025
gene              /gene="bA375F2.1"
                    /pseudo
                    31722..33025
CDS               /gene="bA375F2.1 (similar to UBL1 (ubiquitin-like 1
                    (sentrin)))
                    match: cDNAs: Em:U72722
                    match: ESTs: Em:A19122 Em:A1248769
                    match: proteins: Tr:Q9P08 Tr:O23759 Sw:P55853 Tr:Q92172
                    Sw:Q93068 Sw:P55854 Sw:P55855 Sw:O13351 Sw:Q12306
                    Tr:Q97102 Tr:O57686"
                    /pseudo
                    /codon_start=1
                    /evidence=not_experimental
                    complement(32129..32630)
                    /note="match: GSS: Em:AQ747371"
                    32225..32619
misc_feature       /note="match: GSS: Em:AQ093192"
                    complement(32404..32630)
misc_feature       /note="match: GSS: Em:AQ195587"
                    33174..33222
repeat_region      /note="L2 repeat: matches 2624..2668 of consensus"
                    33291..33725
repeat_region
Query Match      3.5%; Score 22; DB 9; Length 158519;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy              163 TTGAAACAATTTCTACTATA 184
Db              103720 TTGAAACAATTTCTACTATA 103699
RESULT 5
AC141118
LOCUS             AC141118 160961 bp DNA linear HTG 27-MAR-2003
DEFINITION       Rattus norvegicus clone CH230-525P6, WORKING DRAFT SEQUENCE, 40
unordered pieces.
ACCESSION         AC141118
VERSION           AC141118.2 GI:28913318
KEYWORDS          HTG: HTGS PHASE1; HTGS: DRAFT.
SOURCE            Rattus norvegicus (Norway rat)
ORGANISM          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 160961)
REFERENCE
AUTHORS           Murthy,D,Marie, Metzker,M,Lee, Abramson,S, Adams,C, Alder,J.,
Allen,C, Allen,H, Albrooks,S, Amin,A, Anguiano,D,
Anyalebechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H,
Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
Biewald,K, Blair,D, Blankenburg,K, Blyth,P, Brown,M,
Bryant,N, Buhay,C, Burch,P, Burdell,K, Calderon,E,
Cardenas,V, Carter,K, Cavazos,I, Cessari,H, Center,A,
Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D,

```

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Faller, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gevorgyan, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hulys, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., Kang, L., Kovar, C., Kows, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensheve, L., Louisedge, H., Lozano, R.J., Lu, X., Ma, T., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawliny, S., McLeod, M., McNeill, T., Meenan, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackelme, O., Okunnu, G., Olarunpusagbon, A., Pal, S., Parks, K., Pasterak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smaaj, D., Sneed, A., Sodergren, E., Song, X., Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tinney, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooten, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Hol, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 160961)
Worley, K.C.
Direct Submission
Submitted (09-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 160961)
Worley, K.C.
Direct Submission
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Mar 11, 2003 this sequence version replaced gi:28935584.

--- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
--- Project Information
Center project name: KES0
Center clone name: CH230-525P6
--- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap version 0.990329
Consensus quality: 149125 bases at least Q40
Consensus quality: 153679 bases at least Q30
Consensus quality: 157936 bases at least Q20
Estimated insert size: 153783; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1574: contig of 1574 bp in length
1575 1674: gap of unknown length
1675 3680: contig of 2006 bp in length
3681 3780: gap of unknown length
3781 5079: contig of 1299 bp in length
5080 5179: gap of unknown length
5180 7286: contig of 2107 bp in length
7287 7385: gap of unknown length
7386 9577: contig of 2191 bp in length
9578 9677: gap of unknown length
9678 11965: contig of 2288 bp in length
11966 12065: gap of unknown length
12066 14080: contig of 2015 bp in length
14081 14880: gap of unknown length
14881 15944: contig of 1764 bp in length
15945 16044: gap of unknown length
16045 18936: contig of 2892 bp in length
18937 19036: gap of unknown length
19037 21532: contig of 2496 bp in length
21533 21632: gap of unknown length
21633 24022: contig of 2390 bp in length
24023 24122: gap of unknown length
24123 25620: contig of 1498 bp in length
25621 27462: gap of unknown length
27463 27562: contig of 1742 bp in length
27563 30387: gap of unknown length
30388 30487: contig of 2825 bp in length
30488 33253: gap of unknown length
33254 33354: gap of unknown length
33355 35421: contig of 1968 bp in length
35422 38320: gap of unknown length
38321 38419: gap of unknown length
38420 41619: contig of 3199 bp in length
41620 44430: contig of 2712 bp in length
44431 44530: gap of unknown length
44531 47379: contig of 2749 bp in length
47380 47380: gap of unknown length
47381 52261: contig of 4882 bp in length
52262 52361: gap of unknown length
52362 54608: contig of 2247 bp in length
54609 54708: gap of unknown length
54709 57707: contig of 2899 bp in length
57708 57807: gap of unknown length
57809 60363: contig of 2556 bp in length
60364 60463: gap of unknown length
60464 63938: contig of 3475 bp in length
63939 64038: gap of unknown length
64039 67104: contig of 3066 bp in length
67105 67204: gap of unknown length
67205 71666: contig of 4462 bp in length
71667 71766: gap of unknown length
71767 76309: contig of 4543 bp in length
76310 76409: gap of unknown length
76410 81082: contig of 4673 bp in length
81083 81182: gap of unknown length
81183 84621: contig of 3439 bp in length
84622 84721: gap of unknown length
84722 89992: contig of 5271 bp in length
89993 90092: gap of unknown length
90093 95597: contig of 5505 bp in length
95598 95697: gap of unknown length
95698 100812: contig of 5115 bp in length

```

* 100813 100912: gap of unknown length
* 100913 106321: contig of 5409 bp in length
* 106322 106421: gap of unknown length
* 106422 113989: contig of 7568 bp in length
* 113990 114089: gap of unknown length
* 114090 120489: contig of 6400 bp in length
* 120490 120589: gap of unknown length
* 120590 127231: contig of 6642 bp in length
* 127232 127331: gap of unknown length
* 127332 135054: contig of 7723 bp in length
* 135055 135154: gap of unknown length
* 135155 146623: contig of 11469 bp in length
* 146624 146723: gap of unknown length
* 146724 160961: contig of 14238 bp in length.
FEATURES
  source
    1. 160961
       /organism="Rattus norvegicus"
       /mol_type="genomic DNA"
       /db_xref="taxon:10116"
       /clone="CH230-525P6"
BASE COUNT  52694 a 28129 c 28611 g 47601 t 3926 others
ORIGIN
Query Match      3.5%; Score 22; DB 2; Length 160961;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTATTTTTCAGATCATTT 201
Db 113195 CTATATTTTTCAGATCATTT 113216

RESULT 6
BX296535/c 164604 bp DNA linear HTG 02-JUN-2003
LOCUS      Dario rerio clone CH211-234P1, *** SEQUENCING IN PROGRESS ***, 5
DEFINITION unorderd pieces.
ACCESSION  BX296535
VERSION     BX296535.2 GI:30348616
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE     Dario rerio (zebrafish)
ORGANISM   Dario rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
            1 (bases 1 to 164604)
REFERENCE  1 (bases 1 to 164604)
AUTHORS   McJaren, S.
TITLE     Direct Submission
JOURNAL   Submitted (28-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
            On May 2, 2003 this sequence version replaced gi:29335436.
COMMENT   ----- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: zfish-help@sanger.ac.uk
            ----- Project Information
            Center project name: ZC234P1
            ----- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Chemistry: Dye-terminator; 100% of reads
            Consensus quality: 163108 bases at least Q40
            Consensus quality: 163466 bases at least Q30
            Consensus quality: 163645 bases at least Q20
            Insert size: 164204; sum-of-contigs
            Insert size: 159749; 15.3% error; agarose-fp
            Quality coverage: 6.58x in Q20 bases; sum-of-contigs Quality
            coverage: 6.91x in Q20 bases; agarose-fp
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 5 contigs. The true order of the pieces
            * is not known and their order in this sequence record is

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```

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1
* 36553: contig of 36553 bp in length
* 36554 36653: gap of 100 bp
* 36654 58304: contig of 21651 bp in length
* 58305 58404: gap of 100 bp
* 58405 132711: contig of 74307 bp in length
* 132712 132811: gap of 100 bp
* 132812 147096: contig of 14285 bp in length
* 147097 147196: gap of 100 bp
* 147197 164604: contig of 17408 bp in length.
FEATURES
  source
    1. 164604
       /organism="Dario rerio"
       /mol_type="genomic DNA"
       /db_xref="taxon:7955"
       /clone="CH211-234P1"
       /clone_1fb="CHOR-211"
BASE COUNT  51202 a 30712 c 30580 g 51710 t 400 others
ORIGIN
Query Match      3.5%; Score 22; DB 2; Length 164604;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 ACAATTTTCTACTATTTT 190
Db 141836 ACAATTTTCTACTATTTT 141815

RESULT 7
AL356425/c 183901 bp DNA linear HTG 10-JUL-2001
LOCUS      Homo sapiens chromosome 6 clone RP11-390H10, *** SEQUENCING IN
DEFINITION PROGRESS ***, 14 unorderd pieces.
ACCESSION  AL356425
VERSION     AL356425.5 GI:9863770
KEYWORDS   HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1
REFERENCE  1
AUTHORS   Sims, S.
TITLE     Direct Submission
JOURNAL   Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
            On Aug 21, 2000 this sequence version replaced gi:9213882.
            -----
            Center: Sanger Centre

```

Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk

 Project Information
 Center project name: BA390H10

 Summary Statistics
 Sequencing program: XGAP4; version 4.5
 Sequencing vector: Plasmid; 108752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 43% of reads
 Chemistry: Dye-terminator ABI; 13% of reads
 Chemistry: Dye-terminator ABI; 42% of reads
 Consensus quality: 176464 bases at least Q40
 Consensus quality: 179210 bases at least Q30
 Consensus quality: 180657 bases at least Q20
 Insert size: 182601; sum-of-contigs
 Insert size: 195711; 10.1% error; agarose-fp
 Quality coverage: 6.80x in Q20 bases; sum-of-contigs Quality
 Coverage: 8.70x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 14 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1      4652: contig of 4652 bp in length
*      4653      4752: gap of 100 bp
*      4753      10980: contig of 6228 bp in length
*      10981      11080: gap of 100 bp
*      11081      23147: contig of 12067 bp in length
*      23148      23247: gap of 100 bp
*      23248      26829: contig of 3582 bp in length
*      26830      26929: gap of 100 bp
*      26930      29454: contig of 2525 bp in length
*      29455      29554: gap of 100 bp
*      38902      38902: contig of 9348 bp in length
*      38903      39002: gap of 100 bp
*      39003      150562: contig of 11560 bp in length
*      150662      150662: gap of 100 bp
*      150663      153078: contig of 2416 bp in length
*      153079      153178: gap of 100 bp
*      153179      158533: contig of 5355 bp in length
*      158534      158633: gap of 100 bp
*      158634      161010: contig of 2377 bp in length
*      161011      161110: gap of 100 bp
*      161111      164104: contig of 2994 bp in length
*      164105      164204: gap of 100 bp
*      164205      173216: contig of 9012 bp in length
*      173217      173316: gap of 100 bp
*      173317      178295: contig of 4979 bp in length
*      178296      178395: gap of 100 bp
*      178396      183901: contig of 5506 bp in length.
  
```

FEATURES

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source
  1..183901
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /chromosome="6"
    /clone="RP11-390H10"
    /clone_1fb="RP11-11.2"
    1..4652
      /note="assembly_fragment:03969
      clone end:17
      vector_side:left"
      4753..10980
        /note="assembly_fragment:00460
        fragment_chain:1"
        11081..23147
          /note="assembly_fragment:00746
          fragment_chain:1"
        23248..26829
  
```

```

misc_feature /note="assembly_fragment:04384
             fragment_chain:2"
             26930..29454
             /note="assembly_fragment:01338
             fragment_chain:2"
             29555..38902
             /note="assembly_fragment:00073.0"
             39003..150562
             /note="assembly_fragment:00200.0"
             150663..153078
             /note="assembly_fragment:00219"
             153179..158533
             /note="assembly_fragment:00251"
             158634..161010
             /note="assembly_fragment:00513"
             161111..164104
             /note="assembly_fragment:01982"
             164205..173216
             /note="assembly_fragment:02741"
             173317..178295
             /note="assembly_fragment:02844"
             178396..183901
             /note="assembly_fragment:03632"
misc_feature 57024 a 32652 c 34405 g 58512 t 1304 others
BASE COUNT
ORIGIN
Query Match 3.5%; Score 22; DB 2; Length 183901;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  
```

```

Oy      228 ATATGCTTATTTATTTATGTT 249
         |||||
Db      131164 ATATGCTTATTTATTTATGTT 131163
  
```

```

RESULT 8
AC135412
LOCUS
DEFINITION
  Rattus norvegicus clone CH230-4M1, ** SEQUENCING IN PROGRESS **
ACCESSION
  AC135412
VERSION
  HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
KEYWORDS
  Rattus norvegicus (Norway rat)
SOURCE
  ORGANISM
    Rattus norvegicus
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
      Rattus.
      1 (bases 1 to 250935)
  
```

```

REFERENCE
  AUTHORS
    Muzny, D., Marie, Metzker, M., Lee, S., Adams, C., Alder, J.,
    Allen, C., Allen, H., Aliebrooke, S., Amin, A., Angiano, D.,
    Anyalbechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
    Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
    Blawie, K., Blair, D., Blankenburg, K., Blyth, P., Brown, M.,
    Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
    Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,
    Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
    Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
    Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinu, H., Divya, K.,
    Diaper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
    Egan, A., Escotto, M., Eugene, C., Evans, C., Falle, T., Fan, G.,
    Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
    Fraser, C., Gabris, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
    Georegeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
    Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
    Hernandez, R., Hines, S., Hladun, S., Hodgson, A., Hognes, M.,
    Hollins, B., Howells, S., Hu, Y., Hume, J., Idlebird, D., Jackson, A.,
    Jackon, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
    Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
    Kowis, C., Kraft, C., L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
    Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, D.,
  
```


Lorensheva, L., Louised, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathew, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundaasa, M., Murphy, M., Nair, L., Nankervill, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokedi, O., Okwou, G., Olarnunagoon, A., Pal, S., Parks, K., Paternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poldrecker, A., Popovic, D., Prims, E., Pu, L., Puzo, M., Quiroz, J., Rachin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemari, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wiczysk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G., and Gibbs, R. A.

Unpublished
Direct Submission
2 (bases 1 to 250935)
Rat Genome Sequencing Consortium.
Submitted (15-OCN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 250935)
Rat Genome Sequencing Consortium.
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24942076.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GAXY
Center clone name: CH230-4M1

----- Summary Statistics
Assembly program: Atlas;
Consensus quality: 14854 bases at least Q40
Consensus quality: 15473 bases at least Q20
Consensus quality: 15832 bases at least Q20
Estimated insert size: 147873; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 5743: contig of 5743 bp in length
5744 5843: gap of unknown length
5844 44807: contig of 38964 bp in length
44808 44907: gap of unknown length
44908 44908: contig of 6321 bp in length
51228 51328: gap of unknown length
51329 230560: contig of 179232 bp in length
230561 230561: gap of unknown length
230561 234274: contig of 3614 bp in length
234275 234275: gap of unknown length
234275 245739: contig of 11365 bp in length
245740 245839: gap of unknown length
245840 245869: contig of 1030 bp in length
245870 246969: gap of unknown length
246970 248471: contig of 1502 bp in length
248472 248571: gap of unknown length
248572 248572: contig of 1181 bp in length
248573 248582: gap of unknown length
248583 250935: contig of 1083 bp in length.

FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-4M1"
1..1739
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5844..7590
/note="wgs contig"
41966..44807
/note="wgs contig"
44908..47234
/note="wgs contig"
116578..117961
/note="wgs contig"
209111..210845
/note="wgs contig"
218123..220132
/note="wgs contig"
234375..235653
/note="wgs contig"
BASE COUNT 54579 a 29101 c 28918 g 48007 t 90330 others
ORIGIN

Query Match 3.5%; Score 22; DB 2; Length 250935;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 CTATATTTTACAGATCATTT 201
DB 24484 CTATATTTTACAGATCATTT 244505

RESULT 9
AC096515/c 286790 bp DNA linear HTG 09-NOV-2002
LOCUS Rattus norvegicus clone CH230-5A2, *** SEQUENCING IN PROGRESS ***
DEFINITION 9 unordered pieces.
ACCESSION AC096515.5 GI:24818491
VERSION AC096515.5
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 286790)
Muzny, D., Marie, J., Metzger, M., Lee, J., Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bismato, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryan, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Gervais, M., Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hu, Y., Hume, J., Idlebird, D., Jackson, A., Jackson, B., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenzuela, L., Louisedge, H., Lozano, R.J., Lu, X., Ma, U., Maheshwari, M., Maindarte, M., Mahmoud, M., Mallory, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martinez, R., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Mloavajevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nait, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackelmen, O., Okumu, G., Olarnpusagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankoch, C., Plopper, F., Polndexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quirroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reich, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sanders, W., Savery, G., Scheer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajd, D., Sheeh, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soosa, D., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tinney, A., Trejos, Z., Uman, K., Valsar, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yan, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, S., Zhao, S., Dunn, D., von Weinstock, G., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

TITLE REFERENCE AUTHORS JOURNAL

Unpublished
2 (bases 1 to 286790)
Worley, K.C.
Direct Submission
Submitted (18-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS
JOURNAL
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Nov 9, 2002 this sequence version replaced gi:22772011.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GAZY
Center clone name: CH230-5A2
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 79420 bases at least Q40
Consensus quality: 83499 bases at least Q30
Consensus quality: 86426 bases at least Q20
Estimated insert size: 70782; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a working draft sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 216997: contig of 216997 bp in length
* 216998 217097: gap of unknown length
* 217098 248339: contig of 31242 bp in length
* 248340 248439: gap of unknown length
* 248440 258863: contig of 10424 bp in length
* 258864 258963: gap of unknown length
* 258964 263217: contig of 4253 bp in length
* 263217 263316: gap of unknown length
* 263316 281803: contig of 18487 bp in length
* 281804 281903: gap of unknown length
* 281904 283051: contig of 1148 bp in length
* 283052 283151: gap of unknown length
* 283152 284195: contig of 1044 bp in length
* 284196 284295: gap of unknown length
* 284296 285440: contig of 1145 bp in length
* 285441 285540: gap of unknown length
* 285541 286790: contig of 1250 bp in length.

FEATURES
source
1..286790
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-5A2"
2439..2951

misc_feature
/note="clone_boundary
clone_end:17
site:ECORI
end_sequence: BH334013"
19424..20864
/note="wgs contig"
175176..175894
/note="clone_boundary
clone_end:5p6
site:ECORI
end_sequence: BH334015"
177823..179284
/note="wgs end-extension
clone_end:5p6
183835..184861
/note="wgs end-extension
clone_end:5p6"
185363..186393
/note="wgs end-extension
clone_end:5p6"
197893..199394

```

/note="wgs_end_extension
clone_end:Sp6"
215431. .216997
/note="wgs_end_extension
clone_end:Sp6"
217098. .218581
/note="wgs_end_extension
clone_end:Sp6"
220322. .221556
/note="wgs_end_extension
clone_end:Sp6"
246596. .248339
/note="wgs_end_extension
clone_end:Sp6"
248440. .249824
/note="wgs_end_extension
clone_end:Sp6"
258964. .260512
/note="wgs_end_extension
clone_end:Sp6"
266700. .269279
/note="wgs_end_extension
clone_end:Sp6"
273808. .275227
/note="wgs_end_extension
clone_end:Sp6"

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| | | | | | | |
|----|--------|-----------------------|----------------|---------------|----------|---------------|
| | | Query Match | 3.5% | Score 22 | DB 2 | Length 286790 |
| | | Best Local Similarity | 100.0% | Pred. No. 1.2 | | |
| | | Matches 22 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| Qy | 180 | CTATATTTCACGATCATTT | 201 | | | |
| | | | | | | |
| Db | 267793 | CTATATTTTAAAGATCATTT | 267772 | | | |

| | |
|------------|--|
| RESULT 10 | |
| AC013856 | |
| LOCUS | AC013856 44284 bp DNA linear HTG 16-NOV-1999 ***. |
| DEFINITION | Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***. |
| ACCESSION | AC013856 |
| VERSION | AC013856.1 GI:6437479 |
| KEYWORDS | HTG, HTGS_PHASE2. |
| SOURCE | Drosophila melanogaster (fruit fly) |
| ORGANISM | Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 44284) Adams,M. and Venter,J.C. Direct Submission Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA |
| COMMENT | This sequence was identified as CDM:10211564 by the submitter. For further information on this sequence e-mail to fly@celera.com. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved. |
| FEATURES | Location/Qualifiers |
| source | 1..44284 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" |
| BASE COUNT | 13028 a 3444 c 9570 g 12242 t |
| ORIGIN | |

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Query Match      3.4%; Score 21; DB 2; Length 44264;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

| Qy | 345 | TACCAAGTTTTAAATTAA | 365 |
|----|-------|--------------------|-------|
| Db | 40289 | TACCAAGTTTTAAATTAA | 40309 |

| LOCUS | AC020373 | RESULT 11 |
|------------|--|-----------|
| DEFINITION | AC020373 | |
| VERSION | AC020373.1 | |
| KEYWORDS | HTG, HTGS, PHASE2. | |
| SOURCE | Drosophila melanogaster (fruit fly) | |
| ORGANISM | Drosophila melanogaster | |
| REFERENCE | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. | |
| AUTHORS | 1 (bases 1 to 60164) | |
| TITLE | Adams, M. and Venter, J. C. | |
| JOURNAL | Direct Submission | |
| COMMENT | Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA. | |
| | This sequence was identified as CDM:10212952 by the submitter. For more information on this record e-mail to fly@celera.com. | |
| | * NOTE: This is a 'working draft' sequence. | |
| | * This sequence will be replaced | |
| | * by the finished sequence as soon as it is available and | |
| | * the accession number will be preserved. | |

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source      1. 60164
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             /mol_type="genomic DNA"
             /db_xref="taxon:7227"
BASE COUNT  17290 a 12604 c 12884 g 17386 t
ORIGIN
Query Match 3.4% Score 21; DB 2; Length 60164;
Best Local Similarity 100.0%; Pred. NO. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

| | | | | |
|-----------|------------|---|-------------------|------------------------|
| oy | 504 | AACTTTTACCATTAATTA | 524 | |
| Db | 39804 | AAACTTTTACCATTAATTA | 39824 | |
| RESULT 12 | AL671966/c | AL671966 | 61913 bp | DNA |
| LOCUS | DEFINITION | Human DNA sequence from clone Rpl1-541a8 on chromosome 6, complete sequence. | AL671966.AL445924 | linear PRI 07-FEB-2002 |
| ACCESSION | VERSION | AL671966.1 | GI:18642415 | |
| KEYWORDS | SOURCE | Homo sapiens (human) | | |
| ORGANISM | REFERENCE | Authors | | |
| AUTHORS | TITLE | Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgehire, CB10 1SA, UK. E-mail enquiries: humquey@sanger.ac.uk | | |
| JOURNAL | COMMENT | On Feb 8, 2002 this sequence version replaced gi:13375014. | | |

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=

```

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChxX
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RP3-341D10 is from
the library RPCr-3 constructed by the group of Pieter de Jong. For
further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
RP3-341D10 it may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true right end of clone RP3-341D10 is at 82517 in this
sequence. The true left end of clone RP5-1053B6 is at 47109 in this
sequence. The true right end of clone RP1-146H21 is at 20342 in
this sequence. The true right end of clone L10XNC01-131B10 is at
100 in this sequence.
Location/Qualifiers
1..82517
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP3-341D10"
/clone_lib="RPCr-3"
2573..12600
/clone="14 copies 2 mer 1g 96% conserved"
complement(5744..6585)
/clone="match: GSS: Em:AQ897607"
5903..6393
/clone="UTR33 repeat: matches 1..521 of consensus"
complement(15994..6593)
/clone="match: GSS: Em:AQ282846"
7799..8818
/clone="11MD repeat: matches 27..1017 of consensus"
9132..9697
/clone="11MD repeat: matches 1017..1590 of consensus"
15403..15831
/clone="11P11 repeat: matches 5725..6161 of consensus"
16674..18783
/clone="qJ341D10.1"
/gene="qJ341D10.1"
/product="qJ341D10.1 (novel protein)"
/clone="match: cDNAs: Em:AF116646 Em:AL157483 Em:AK002126
Em:DS2659 Em:DS2659 Em:C01580 Em:A1652628 Em:A1110652
Em:DS2752 Em:DS2671 Em:AW026446 Em:AA773203 Em:AW581342
Em:AW088009 Em:AW025693 Em:A1699487 Em:AA281222
Em:AW440954 Em:A1828021 Em:A1751822 Em:AA079045
Em:AW659871 Em:AF063526 Em:AA043597 Em:Z45941 Em:A1913223
Em:AL049045 Em:A1640587 Em:A1990225 Em:A1356844
Em:AW471241 Em:A1922789 Em:H13398 Em:D79651"
/clone="match: experimental"
16674..17003
/clone="qJ341D10.1"
/clone="match: proteins: Tr:Q9VX59 Tr:O02330 Tr:Q9Y2J5
Tr:Q9V517"
/codon_start=1
/evidence="not_experimental"
/product="qJ341D10.1 (novel protein)"
/protein_id="CD139074.1"
/db_xref="GI:17736645"
/translat="MTCCVRSDFLLIGRFDVKVKGSGDVLHCCKYLHDDLIVITPP
VTGIFHLMPERKCADELTPEDQIRMTCIQSKAINEASRSHLGMLVFRREIEITHLKQAYR
TNSAEAVG"

```

```

polyA_signal      18778..18783
/gene="dJ341D10.1"
repeat_region     20672..20723
/note="26 copies 2 mer aa 73% conserved"
repeat_region     22455..22572
/note="59 copies 2 mer aa 61% conserved"
repeat_region     23789..25430
/note="WSTA-internal repeat: matches 2..1651 of consensus"
repeat_region     26627..26777
/note="MER58C repeat: matches 44..87 of consensus"
repeat_region     30005..30234
/note="MER5 repeat: matches 1..237 of consensus"
misc_feature      31771..32971
/note="Cpg island"
/evidence=not_experimental
misc_feature      32175..33183
/note="1372bp of IS186 (X03123) excised: This sequence
represents the duplicated flanking sequence of the IS186."
misc_feature      32299
/note="Tandem repeat. Forced join. Gap size estimated to
be approximately 850bp by BAMH1 and ECOR1 restriction
enzyme digest data."
misc_feature      complement(32350..32388)
/note="Tandem repeat. Single clone region"
misc_feature      complement(32497..32922)
/note="match: GSS: Em:AQ473058"
repeat_region     33793..33848
/note="28 copies 2 mer tc 73% conserved"
repeat_region     36506..36833
/note="L1M43 repeat: matches 5975..6300 of consensus"
repeat_region     37145..37613
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misc_feature      41221..41505
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repeat_region     41932..41973
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/note="match: GSS: Em:B99529"
gene             45131..45380
/gene="dJ341D10.2"
<45131..>45380
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Sw:P41275 Tr:Q9W389 Sw:P40617"
/codon_start=3
/evidence=not_experimental
/product="dJ341D10.2 (similar to ADP ribosylation factor
3)"
/protein_id="CAD19075.1"
/db_xref="GI:17736646"
/translation="LPSKTDHCKMSKSLTTLIDYELSIYDNGDLKGRAMPYVAA
AHGLVFDSSDIDRMQEVKILTHLSDSKVAKPIL"
misc_feature      47478..47613
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misc_feature      47953..48394
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repeat_region     48316..48343
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repeat_region     51272..51632
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misc_feature      52831..53269
/note="match: GSS: Em:AQ210994"
complement(53421..53946)
/note="match: GSS: Em:AQ666879"
misc_feature      53958..54526
/note="match: GSS: Em:AQ483633"
55574..56018
/note="L1M44 repeat: matches 5833..6294 of consensus"
61332..61798
/note="UTR32 repeat: matches 15..471 of consensus"
63634..63884
/note="AluI/mcmonmer repeat: matches 249..299 of consensus"
66278..66509

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repeat_region     68116..68508
/note="TIGGER1 repeat: matches 2174..2410 of consensus"
/note="MER74B repeat: matches 128..548 of consensus"
gene             complement(69768..81526)
/gene="dJ341D10.3"
complement(join(69768..70171,78435..78534,78748..78867,
79951..80026,80467..80779,81432..81526))
/gene="dJ341D10.3"
/product="dJ341D10.3 (similar to HpaII tiny fragments
locus 9C (HTF9C))"
/note="match: cDNAs: Em:X56044
match: ESTs: Em:W39709 Em:A1192958 Em:AA749428 Em:AA721368
Em:AA373290 Em:W15487 Em:W52823 Em:A1765573 Em:AA091456"
/evidence=not_experimental
complement(join(70045..70171,78435..78534,78748..78867,
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/gene="dJ341D10.3"
/note="match: proteins: Tr:P70222"
/codon_start=1
/evidence=not_experimental
/product="dJ341D10.3 (similar to HpaII tiny fragments
locus 9C (HTF9C))"
/protein_id="CAD19076.1"
/db_xref="GI:17736647"
/translation="BELHVQKEIVKEFFIRPGACGLTSLYFQESTMTTRCSHQSPY

Query Match      3.4%; Score 21; DB 9; Length 82517;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              173 TTTTCTACTATATTTTACAG 193
Db              70852 TTTTCTACTATATTTTACAG 70832

RESULT 14
AC005449
LOCUS
DEFINITION
Drosophila melanogaster, chromosome 2R, region 44C4-44C5, Pl clone
DS06765, complete sequence.
ACCESSION
AC005449
VERSION
AC005449.1 GI:4056408
SOURCE
HTG.
ORGANISM
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 85518)
REFERENCE
Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Brenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Fartan,D.E., Galle,R., George,R.A., Harris,L.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Kaira,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomoton,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacle,J.M., Park,S.,
Pfeiffer,B., Poon,L., Punch,E., Sequeira,A., Sethi,H., Snir,E.,
Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R.,
Zieran,L.L. and Rubin,G.M.
Sequencing of Drosophila chromosome 2R, region 44C4-44C5
2 (bases 1 to 85518)
Unpublished (1998)
TITLE
Drosophila chromosome 2R, region 44C4-44C5
JOURNAL
REFERENCE
AUTHORS
Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chavez,C.,
Chew,M., Doyle,C.M., Fartan,D.E., Fianagan,J., Houston,K.A.,
Hummasti,S.R., Kaira,K., Kearney,L., Kim,S.H., Lee,B.,
Lomoton,M.A., Mak,J., Mazda,P., Mok,M.S., Moshrefi,A.R.,
Moshrefi,M., Nixon,K., Pacle,J.M., Park,S., Pfeiffer,B., Punch,E.,
Snir,E., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R.,
Zieran,L.L. and Kimmel,B.E.
DIRECT SUBMISSION
Submitted (14-AUG-1998) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Dec 23, 1998 this sequence version replaced gi:4049302.
COMMENT

```

Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720

For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (<http://www.fruitfly.org/sequence/>) or send email
to bdg@fruitfly.berkeley.edu.
Pl library location: 71-45.

FEATURES

source

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Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="y2; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2R"
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/clone="P1 DS06765 (D363)"
/clone_1ib="P1 library, partial Sau3A in pAd10sacB11"
BASE COUNT 24282 a 17889 c 18642 g 24705 t
ORIGIN

Query Match 3.4%; Score 21; DB 3; Length 85518;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 AACCTTTTACCATATATTA 524
Db 75739 AACCTTTTACCATATATTA 75759

RESULT 15
AL354827/c 127641 bp DNA linear PRI 28-JAN-2001
LOCUS Human DNA sequence from clone RP11-280J7 on chromosome 13, complete
DEFINITION sequence.
ACCESSION AL354827 AC025666
VERSION AL354827.5 GI:12597080
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homimidae; Homo.
1 (bases 1 to 127641)
Blakey, S.
Direct Submission
Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On or before May 15, 2001 this sequence version replaced
GI:1387396, GI:12539586.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone configs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr13>
RP11-280J7 is from the library RPc1-11.1 constructed by the group
of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-280J7 it may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-280J7 is at 127641 in this
sequence. The true right end of clone RP11-475P14 is at 100 in this
sequence.

FEATURES

source

1..127641
Location/Qualifiers
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BASE COUNT 41986 a 21749 c 21502 g 42404 t
ORIGIN

Query Match 3.4%; Score 21; DB 9; Length 127641;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 AGTAAATTAAATATATATAA 390
Db 33240 AGTAAATTAAATATATATAA 33220

RESULT 16
AC080184/c 147078 bp DNA linear HTG 24-AUG-2002
LOCUS Homo sapiens chromosome 13 clone RP11-601J15 map 13, WORKING DRAFT
DEFINITION SEQUENCE, 24 unordered pieces.
ACCESSION AC080184 GI:11094827
VERSION AC080184.2
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homimidae; Homo.
1 (bases 1 to 147078)
Birren, B.; Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 13, clone RP11-601J15
Unpublished
2 (bases 1 to 147078)
Birren, B.; Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Barna, N., Baetsen, V., Beda, F., Boguslavsky, U.,
Boukhalter, B., Brown, A., Burkett, G., Campoliano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dextrallano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,
FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
Graham, L., Grand-Pierre, N., Hago, B., Heatford, A., Horton, L.,
Iliev, I., Johnson, R., Jones, C., Kam, L., Karadas, A., Lakoque, K.,
Lamazeres, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K.,
McSheehers, R., Meldrum, J., Meneus, L., Mihova, C.H., Mlenga, V.,
Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,
O'Donnell, P., O'Neill, D., Oliver, R.M., Oliver, J., Peterson, K.,
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,
Rogov, P., Rothen, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
Sougner, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wymann, D., Ye, W.-J., Young, G., Zainoun, J.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (28-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147078)

TITLE
JOURNAL
REFERENCE
AUTHORS
Anderson, S., Barna, N., Baetsen, V., Beda, F., Boguslavsky, U.,
Boukhalter, B., Brown, A., Burkett, G., Campoliano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dextrallano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,
FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
Graham, L., Grand-Pierre, N., Hago, B., Heatford, A., Horton, L.,
Iliev, I., Johnson, R., Jones, C., Kam, L., Karadas, A., Lakoque, K.,
Lamazeres, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K.,
McSheehers, R., Meldrum, J., Meneus, L., Mihova, C.H., Mlenga, V.,
Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,
O'Donnell, P., O'Neill, D., Oliver, R.M., Oliver, J., Peterson, K.,
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,
Rogov, P., Rothen, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
Sougner, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wymann, D., Ye, W.-J., Young, G., Zainoun, J.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (28-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147078)

TITLE
JOURNAL
COMMENT

DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
 Fitzhigh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
 Grahm,L., Grand-Pierre,N., Hagos,B., Hearford,A., Horton,L.,
 Iliev,I., Johnson R., Jones,C., Kann,L., Karatas,A., Labocque,K.,
 Lamazares,R., Landers,T., Lenoczky,J., Levine,R., Liu,C., Liu,G.,
 MacDonald,P., Marquis,N., McArthur,M., McEwan,P., McEwan,K.,
 McKeete,R., Meldrum,J., Menus,L., Mhova,T., Mleaga,V.,
 Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
 O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,
 Pierre,N., Pisaní,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
 Rogov,P., Rochman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
 Sougnaz,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Straus,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Titrrell,A., Travers,M., Trigglio,J., Vassiliev,H., Viel,R., Vo,A.,
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
 Zimmer,A. and Zody,M.

Direct Submission
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Nov 4, 2000 this sequence version replaced gi:10334904.
 All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Genome Center

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: 601_J_15

Center clone name: 601_J_15

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye, 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 137099 bases at least Q40

Consensus quality: 142162 bases at least Q30

Consensus quality: 143831 bases at least Q20

Insert size: 172000; agarose-fp

Insert size: 144778; sum-of-contigs

Quality coverage: 3.4 in Q20 bases; agarose-fp

Quality coverage: 4.0 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
 consists of 24 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 18712: contig of 18712 bp in length
 * 18713 18812: gap of 100 bp
 * 18813 20419: contig of 1607 bp in length
 * 20420 20519: gap of 100 bp
 * 20520 21760: contig of 1241 bp in length
 * 21761 21860: gap of 100 bp
 * 21861 23353: contig of 1493 bp in length
 * 23354 23453: gap of 100 bp
 * 23454 25619: contig of 2166 bp in length
 * 25620 25719: gap of 100 bp
 * 25720 27181: contig of 1462 bp in length
 * 27182 27281: gap of 100 bp
 * 27282 29012: contig of 1731 bp in length
 * 29013 29112: gap of 100 bp
 * 29113 33172: contig of 4060 bp in length
 * 33173 33273: gap of 100 bp
 * 33274 37412: contig of 4040 bp in length
 * 37413 42066: gap of 4654 bp in length
 * 42067 42166: gap of 100 bp
 * 42167 46649: contig of 4483 bp in length
 * 46650 46749: gap of 100 bp

FEATURES
source

46750 50665: contig of 3916 bp in length
 * 50666 50765: gap of 100 bp
 * 50766 56271: contig of 5506 bp in length
 * 56272 56371: gap of 100 bp
 * 56372 60600: contig of 4229 bp in length
 * 60601 60700: gap of 100 bp
 * 60701 65226: contig of 4526 bp in length
 * 65227 65326: gap of 100 bp
 * 65327 71627: contig of 6300 bp in length
 * 71628 71727: gap of 100 bp
 * 71728 79581: contig of 7855 bp in length
 * 79582 79681: gap of 100 bp
 * 79682 90103: contig of 10422 bp in length
 * 90104 90203: gap of 100 bp
 * 90204 98835: contig of 8632 bp in length
 * 98836 98935: gap of 100 bp
 * 98936 107000: contig of 8065 bp in length
 * 107001 107100: gap of 100 bp
 * 107101 117126: contig of 10026 bp in length
 * 117127 117226: gap of 100 bp
 * 117227 129147: contig of 11921 bp in length
 * 129148 129247: gap of 100 bp
 * 129248 146388: contig of 17141 bp in length
 * 146389 146488: gap of 100 bp
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19364..19786,19905..19941))
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HIRA protein (Fragment)"
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TTNGGILSTLONNRKINSITNNITNNSQOQOQOQPSVNSKILTRIGALSEVNSD
TSLFKOLMLAQVLESLEYHMLITTKYVINCIVKLTDLTDLTGLGSTLNDH
HHHHHHNNHTKSNMESNPFNSNLSIPWESITLGLSKRSLKELPLTMAKNTLORM
VQGFESINAFSKNLLVDFDTLNRK"
join(20447..20501,20627..22015,22131..23077)
/notice="Geneid exon scores (in order of location ranges) :
-2.34, 73.78, 62.73 - GSCJ_ID dd_00126"
/codon_start=1
/product="similar to Plasmodium falciparum (Isolate 3D7) .
Asparagine-rich antigen"
/protein_id="AA052408.1"
/db_xref="GI:28829917"
/translation="MMGLILFENSPLOVYLOSILNKENEDRGVLSFEMFSQNI
NNEBYNQIKYNNNNKNNNNNTFKKNNKNNKIKNKQIFPMSLYQSIISITIE
SDILVQSPFIQNPNSLKQDNDDDDESPPIYPLSLTLDLNDNNSNNNNKEL
SLNIEISILSYNNNNNNNNNNNNNNNNNNIILISILITISIFLNFLLIFISILIVI

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Query Match 3.4%; Score 21; DB 3; Length 151802;
Beat Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

cy 370 AGTAAATTATATATATAAA 390
Db 1852 AGTAAATTATATATATAAA 1872

RESULT 18
AC006017/c
LOCUS Homo sapiens PAC clone RPS-98107 from 7q34-q36, complete sequence.
DEFINITION AC006017
ACCESSION AC006017
VERSION AC006017.2 GI:4508141
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 162556)
Sullivan, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
MEDLINE 9847074
PUBMED 9847074
2 (bases 1 to 162556)
REFERENCE 2
Joshu, C. and McGaine, B.
The sequence of Homo sapiens PAC clone RPS-98107
Unpublished
3 (bases 1 to 162556)
REFERENCE 3
Waterston, R.H.
Direct Submision
Submitted (22-NOV-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 162556)
REFERENCE 4
Waterston, R.H.
Direct Submision
Submitted (24-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 162556)
REFERENCE 5
Waterston, R.
Direct Submision
Submitted (28-JUL-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 162556)
REFERENCE 6
Waterston, R.
Direct Submision
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 24, 1999 this sequence version replaced gi:3907501.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu
----- Summary Statistics
-----
Center project name: H_DU0981007

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.
This sequence was finished as follows unless otherwise noted:

```

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

This clone was derived from human PAC library RPCL-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. The clone may be obtained either from Genome Systems, Inc. (<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP4-669117. Actual start of this clone is at base position 1 of RP5-98107; actual end is at 162556 of RP5-98107.

The run of A's from 125217 to 125241 may contain one less A, no read was able to make an exact call.

FEATURES

source Location/Qualifiers

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1..162556
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /chromosome="7"
    /map="7q34-q36"
    /clone="RP5-98107"
    /clone_1fb="RPCL-5"
    8..202
        /rpt_family="L2"
        repeat_region
        668..750
            /rpt_family="L2"
            repeat_region
        760..1053
            /rpt_family="Alu"
            repeat_region
        1131..1425
            /rpt_family="Alu"
            repeat_region
        1575..1748
            /rpt_family="MIR"
            repeat_region
        2524..2623
            /rpt_family="MaLR"
            repeat_region
        2791..2852
            /rpt_family="MaLR"
            repeat_region
        2915..2984
            /rpt_family="L2"
            repeat_region
        2991..3022
            /rpt_family="L1"
            repeat_region
        3023..3051
            /rpt_family="C(AAA)n"
            repeat_region
        3052..3327
            /rpt_family="L1"
            repeat_region
        3328..3599
            /rpt_family="Alu"
            repeat_region
        3600..3992
            /rpt_family="L1"
            repeat_region
        4044..4128
            /rpt_family="MaLR"
            repeat_region
        4300..4321
            /rpt_family="AT-rich"
            repeat_region
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repeat_region 4725..4879
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repeat_region 4920..5210
    /rpt_family="Alu"
misc_feature 5286..5436
    /note="match to EST AI150152 (NID:g3678621) qf44h12.x1"
gene <5287..10444
    /gene="WUGSC:H_DJ0981007.1"
    join(<5287..5436,10289..10444)
    /gene="WUGSC:H_DJ0981007.1"
    /note="similar to glycosyl transferases; similar to CAA22098 (PID:g3980030); H_DJ0981007.1"
    /codon_start=1
    /evidence=not experimental
    /protein_id="A045823.1"
    /db_xref="GI:5630078"
    /translation="IMCGQDFTIPCSRVGHISKQTKSTIISANTHNYRLVH
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5535..5711
    /rpt_family="L1"
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    /rpt_family="Alu"
repeat_region 6341..6386
    /rpt_family="MER1_type"
repeat_region 6663..6766
    /rpt_family="L1"
repeat_region 6767..7063
    /rpt_family="Alu"
repeat_region 7064..7395
    /rpt_family="L1"
repeat_region 7396..7709
    /rpt_family="Alu"
repeat_region 7710..7729
    /rpt_family="L1"
repeat_region 7730..8077
    /rpt_family="MER2_type"
repeat_region 8078..8202
    /rpt_family="L1"
repeat_region 8357..8483
    /rpt_family="L1"
repeat_region 8484..8786
    /rpt_family="Alu"
repeat_region 8787..9101
    /rpt_family="L1"
repeat_region 9817..9905
    /rpt_family="MIR"
misc_feature 10284..10499
    /note="match to EST AA907643 (NID:g3043103) om30c11.s1"
misc_feature 10289..10485
    /note="match to EST AI150152 (NID:g3678621) qf44h12.x1"
repeat_region 11036..11308
    /rpt_family="Alu"
repeat_region 11673..11730
    /rpt_family="L2"
repeat_region 11731..12032
    /rpt_family="Alu"
repeat_region 12279..12291
    /rpt_family="Alu"
repeat_region 12292..12595
    /rpt_family="Alu"
repeat_region 12596..12771
    /rpt_family="Alu"
repeat_region 12870..12924
    /rpt_family="TA)n"
repeat_region 13449..13583
    /rpt_family="MIR"
repeat_region 13610..13693
    /rpt_family="MER53"
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Query Match 3.4%; Score 21; DB 9; Length 162556;
Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 234 TTTATTTATTTATGTTGCTCA 254
 Db 44465 TTTATTTATTTATGTTGCTCA 44445

RESULT 19
 AL646050 164018 bp DNA linear ROD 14-MAR-2002
 LOCUS Mouse DNA sequence from clone RP23-460G5 on chromosome 11, complete
 DEFINITION
 ACCESSION AL646050
 VERSION AL646050
 KEYWORDS HTG.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE 1 (bases 1 to 164018)
 JOURNAL Direct Submission
 AUTHORS Submitted (14-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 COMMENT On Mar 21, 2002 this sequence version replaced gi:19309548. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

COMMENT

This sequence was either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-460G5 is from the RP23-23 Mouse PAC library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: DBAC63.6
 IMPORTANT: This sequence is not the entire insert of clone RP23-460G5. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP23-460G5 is at 164018 in this sequence. The true right end of clone RP23-298113 is at 2000 in this sequence.

FEATURES

source
 1. 164018
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="11"
 /clone="RP23-460G5"
 /clone_1id="RP23-23"
 /clone_1id="RP23-23"
 /clone_1id="RP23-23"
 /note="Sequence confirmed by mouse whole genome shotgun supercontig data sequenced by the Mouse Genome Sequencing Consortium, contig 126003215, version 1."
 misc_feature
 63783..63798
 /note="Sequence confirmed by mouse whole genome shotgun supercontig data sequenced by the Mouse Genome Sequencing Consortium, contig 126003215, version 1."
 BASE COUNT 50254 a 31520 c 32168 g 50076 t
 ORIGIN

Query Match 3.4%; Score 21; DB 10; Length 164018;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 234 TTTATTTATTTATGTTGCTCA 254
 Db 9573 TTTATTTATTTATGTTGCTCA 9593

RESULT 20
 AC021838 166438 bp DNA linear HTG 04-APR-2000
 LOCUS Homo sapiens chromosome 6 clone RP11-4L15 map 6, WORKING DRAFT
 DEFINITION
 ACCESSION AC021838
 VERSION AC021838.3
 KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE 1 (bases 1 to 166438)
 JOURNAL Homo sapiens chromosome 6, clone RP11-4L15
 REFERENCE
 AUTHORS 2 (bases 1 to 166438)
 Birren, B., Hinton, L., Nusbaum, C., Lander, E., Abrahams, H., Allen, N., Anderson, S., Baldwin, D., Barna, N., Beckwith, R., Beda, F., Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choe, Y., Collins, M., Collins, S., Collymore, A., Cooke, P., Dekrell, A., Dewar, K., Domino, M., Doyle, M., Fennell, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heath, A., Horton, L., Howland, J., Johnson, R., Jones, C., Kahn, L., Karas, A., Klein, J., Landers, J., Lechoczy, J., Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K., McNeister, R., Meldrum, J., Meneses, L., Morrow, J., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P., Oliver, T., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange, T., Thomas, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vasilev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., J., Zimmer, A. and Zody, M.

TITLE
 JOURNAL Direct Submission
 COMMENT Submitted (20-CHAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02144, USA
 On Apr 4, 2000 this sequence version replaced gi:16984455.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIRB
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L6010
 Center clone name: 4_L15
 ----- Summary Statistics
 Sequencing Vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phred; version 0.960731
 Consensus quality: 159804 bases at least Q40
 Consensus quality: 162919 bases at least Q30
 Consensus quality: 164262 bases at least Q20
 Insert size: 167000; agarose-fp
 Insert size: 165238; sum-of-coverage
 Quality coverage: 4.5 in Q20 bases; agarose-fp
 Quality coverage: 4.5 in Q20 bases; sum-of-coverage

 * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will

```

* be preserved.
1 1110: contig of 1110 bp in length
* 1111 1210: gap of 100 bp
* 1211 2074: contig of 864 bp in length
* 2075 2174: gap of 100 bp
* 2175 4720: contig of 2546 bp in length
* 4721 4820: gap of 100 bp
* 4821 8287: contig of 3467 bp in length
* 8288 8387: gap of 100 bp
* 8388 13431: contig of 5044 bp in length
* 13432 13531: gap of 100 bp
* 13532 21554: contig of 8023 bp in length
* 21555 34613: contig of 12959 bp in length
* 34614 34713: gap of 100 bp
* 34714 46970: contig of 12257 bp in length
* 46971 47071: gap of 100 bp
* 47071 62608: contig of 15538 bp in length
* 62609 62708: gap of 100 bp
* 62709 78889: contig of 16180 bp in length
* 78890 103384: contig of 24396 bp in length
* 103385 103484: gap of 100 bp
* 103485 134361: contig of 30877 bp in length
* 134362 134461: gap of 100 bp
* 134462 166438: contig of 31977 bp in length.
FEATURES
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1. 166438
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6"
/clone="RP11-4L15"
/clone_lib="RPCT-11 Human Male BAC"
1. 1110
/feature="assembly_fragment"
1211. 2074
/feature="assembly_fragment"
clone_end:sp6
vector_side:right"
2175. 4720
/feature="assembly_fragment"
4821. 8287
/feature="assembly_fragment"
8388. 13431
/feature="assembly_fragment"
13532. 21554
/feature="assembly_fragment"
21655. 34613
/feature="assembly_fragment"
34714. 46970
/feature="assembly_fragment"
47071. 62608
/feature="assembly_fragment"
62709. 78888
/feature="assembly_fragment"
78989. 103384
/feature="assembly_fragment"
103485. 134361
/feature="assembly_fragment"
134462. 166438
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vector_side:right"

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BASE COUNT 49284 a 32025 c 31847 g 52054 t 1228 others

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 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

272 TGATGCCAATATCTTTTA 292

Db 156305 TGATGCCAATATCTTTTA 156325

RESULT 21

AC008187

LOCUS

DEFINITION

AC008187

AC008187

AC008187

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Query Match 3.4%; Score 21; DB 3; Length 168417;
 BASE COUNT 49778 a 35463 c 34694 g 48482 t

TITLE JOURNAL
 REFERENCE AUTHORS
 Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Fartan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummel, S.R., Katta, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomoth, M.A., Mazda, P., Moshirefi, A.R., Moshirefi, M., Nixon, K., Paclet, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snit, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M.
 Direct Submission
 Submitted (29-JUL-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
 On Mar 10, 2001 this sequence version replaced gi:7259657.
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory, MS 64-121
 Berkeley, CA 94720
 This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this BAC and its neighboring clones, and relationship to other sequences, please visit our sequence archive Web site (<http://www.fruitfly.org/sequence/>) or send email to hdg@fruitfly.berkeley.edu.
 Location/Qualifiers
 1. 168417
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="Y; cn bw sp"
 /db_xref="taxon:7227"
 /chromosome="2R"
 /map="47D-47E"
 /clone="BACR13D20 (D604)"
 /clone_lib="RPCT-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI in pBAC3.6)"

Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 345 TACAAGGTTTAAATTAA 365
Db 9599 TACAAGGTTTAAATTAA 96019

RESULT 22
AC114655/c
LOCUS
DEFINITION Mus musculus clone RP24-160J12, WORKING DRAFT SEQUENCE, 5 ordered
pieces.
AC114655
AC114655.4 GI:24182179
HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP24-160J12
JOURNAL
REFERENCE
AUTHORS Unpublished
2 (bases 1 to 174595)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Baran, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalil, B., Brown, A., Camarata, J., Campiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatae, A., Kelle, C., Lacroque, K., Lamazares, R.,
Landers, T., Lehotzky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menus, L.,
Milhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnupack, R.,
Seaman, S., Severy, P., Spencer, B., Stenge-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,
Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL
REFERENCE Submitted (10-MAR-2002) Whitehead Institute/MIT Center for Genome
AUTHORS Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 174595)
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Baran, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalil, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafiz, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatae, A., Kelle, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J.,
Matthews, C., McCarthy, M., Meldrim, J., Menus, L., Milhova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R.,
Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnupack, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stenge-Thomann, N.,
Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K.,
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL
REFERENCE Submitted (21-OCT-2002) Whitehead Institute/MIT Center for Genome
AUTHORS Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 21, 2002 this sequence version replaced gi:21362165.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: I24414

Center clone name: 160_J_12

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 172913 bases at least Q40

Consensus quality: 173846 bases at least Q30

Insert size: 163000; agarose-fp

Insert size: 174195; sum-of-contigs

Quality coverage: 12.6 in Q20 bases; agarose-fp

Quality coverage: 11.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 4975: contig of 4975 bp in length
* 4976 5075: gap of 100 bp
* 5076 30323: contig of 25254 bp in length
* 30330 30429: gap of 100 bp
* 30430 70338: contig of 39909 bp in length
* 70339 70438: gap of 100 bp
* 70439 121125: contig of 50687 bp in length
* 121126 121225: gap of 100 bp
* 121226 174595: contig of 5370 bp in length.
Location/Qualifiers

FEATURES

source

1. .174595
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-160J12"
/clone_1lb="RPCI-24 Male Mouse BAC"
1. .4975
/note="assembly_fragment"

misc_feature
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misc_feature
/note="assembly_fragment"

RESULT 23

AL831725/c
LOCUS
AL831725 174712 bp DNA linear ROD 19-SEP-2002

Query Match 3.4%; Score 21; DB 2; Length 174595;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 226 GTATATGCTTATTTATTTAT 246
Db 87083 GTATATGCTTATTTATTTAT 87063

DEFINITION Mouse DNA sequence from clone RP23-106P7 on chromosome X, complete sequence.

ACCESSION AL831725

VERSION AL831725.5 GI:22798440

KEYWORDS HTG.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 174712)

AUTHORS Heath, P.

TITLE Direct Submission

JOURNAL Submitted (19-SEP-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk

COMMENT On Sep 12, 2002 this sequence version replaced gi:22416161.

----- Genome Center -----

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep

RP23-106P7 is from the RPCT-23 Mouse PAC library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6.

Location/Qualifiers

1..174712

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="X"

/clone="RP23-106P7"

/clone_1fb="RPCT-23"

BASE COUNT 52726 a 34512 c 35016 g 52458 t

ORIGIN

Query Match 3.4%; Score 21; DB 10; Length 174712;

Best Local Similarity 100.0%; Pred. NO. 4.6;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 ATGAGCTAATTATATATAT 386

|||||

Db 91785 ATGAGTAATTAATATATAT 91765

|||||

RESULT 24

AC110071 174902 bp. DNA linear HTG 09-FEB-2002

LOCUS AC110071

DEFINITION Homo sapiens chromosome UNK clone RP13-875011, WORKING DRAFT

SEQUENCE AC110071

AC110071.1 GI:18642891

VERSION AC110071

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 174902)

AUTHORS Waterston, R.H.

TITLE The sequence of Homo sapiens clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 174902)

AUTHORS Waterston, R.H.

TITLE Direct Submission

JOURNAL Submitted (09-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

Contact: submissions@watsn.wustl.edu

----- Project Information -----

Center project name: H_FH0875011

----- Summary Statistics -----

Sequencing vector: M13; 2%

Sequencing vector: Plasmid; 98%

Chemistry: Dye-primer ET; 0% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 171309 bases at least Q40

Consensus quality: 172330 bases at least Q30

Consensus quality: 172787 bases at least Q20

Insert size: 197000; agarose-fp

Insert size: 175023; sum-of-contigs

Quality coverage: 7.55 in Q20 bases; agarose-fp

Quality coverage: 6.37 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1114: contig of 1114 bp in length

1115 1214: gap of unknown length

1215 2396: contig of 1182 bp in length

2397 2496: gap of unknown length

2497 3597: contig of 1101 bp in length

3598 3697: gap of unknown length

3698 6579: contig of 2882 bp in length

6580 6679: gap of unknown length

6680 8469: contig of 1790 bp in length

8470 8569: gap of unknown length

8570 11032: contig of 2463 bp in length

11033 11132: gap of unknown length

11133 15590: contig of 4458 bp in length

15591 15690: gap of unknown length

15691 27937: contig of 12247 bp in length

27938 28037: gap of unknown length

28038 47310: contig of 19273 bp in length

47311 47410: gap of unknown length

47411 68421: contig of 21011 bp in length

68422 68522: gap of unknown length

68522 119833: contig of 51312 bp in length

119834 119933: gap of unknown length

119934 174902: contig of 54969 bp in length.

Location/Qualifiers

1..174902

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="UNK"

FEATURES

source

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misc_feature      /clone="RP13-875011"
                  1..1114
misc_feature      /note="assembly_name:Contig12"
                  1215..2396
misc_feature      /note="assembly_name:Contig23"
                  2497..3597
misc_feature      /note="assembly_name:Contig41"
                  3698..6579
misc_feature      /note="assembly_name:Contig42"
                  6680..8469
misc_feature      /note="assembly_name:Contig43"
                  8570..11032
misc_feature      /note="assembly_name:Contig44"
                  11133..15590
misc_feature      /note="assembly_name:Contig45"
                  15691..27937
misc_feature      /note="assembly_name:Contig46"
                  28038..47310
misc_feature      /note="assembly_name:Contig47"
                  47411..68421
misc_feature      /note="assembly_name:Contig48"
                  68522..119833
misc_feature      /note="assembly_name:Contig49"
                  119934..174902
misc_feature      /note="assembly_name:Contig50"
                  174903..36477
BASE COUNT      54818 a 36387 c 36477 g 46114 t 1106 others
ORIGIN

```

```

Query Match      3.4%; Score 21; DB 2; Length 174902;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      234 TTTATTTATTTATTTGCTCA 254
Db      168010 TTTATTTATTTATTTGCTCA 168030

```

```

RESULT 25
AC117760/c      191470 bp DNA linear HTG 11-MAR-2003
LOCUS
DEFINITION      Mus musculus clone RP24-421023, WORKING DRAFT SEQUENCE, 11
unpublished
ACCESSION      AC117760
VERSION      AC117760.3 GI:28913296
KEYWORDS      HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 191470)
Birten,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP24-421023
Unpublished
2 (bases 1 to 191470)
Birten,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Batra,N., Basile,V., Bloom,T., Bognuslavsky,L.,
Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gold,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Lander,E., Levine,R., Lindblad-Toh,K., Liu,G.,
Lander,T., Lehotzky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,U., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Menus,L.,
Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 191470)
Anderson,S., Arachchi,H.M., Barna,N., Basile,V., Bloom,T.,
Bognuslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Lander,E., Levine,R.,
Lindblad-Toh,K., Liu,G., Liu,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,U., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Menus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 11, 2003 this sequence version replaced gi:28394940.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

```

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L25649
Center clone name: 421_O_23
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 188558 bases at least Q40
Consensus quality: 189590 bases at least Q30
Consensus quality: 189992 bases at least Q20
Insert size: 192000; agarose-fp
Insert size: 190470; sum-of-coverage
Quality coverage: 7.8 in Q20 bases; agarose-fp
Quality coverage: 7.9 in Q20 bases; sum-of-coverage
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
52533: contig of 52533 bp in length
52534
52633: gap of 100 bp
52634
52750: contig of 1117 bp in length
52751
53850: gap of 100 bp
53851
57435: contig of 3585 bp in length
57436
57535: gap of 100 bp
57536
61130: contig of 3595 bp in length
61131
61230: gap of 100 bp
61231
66870: contig of 7640 bp in length
66871
68970: gap of 100 bp
68971
74009: contig of 5039 bp in length

```



```

DEFINITION      Homo sapiens chromosome 6 clone RP11-763J6, WORKING DRAFT SEQUENCE
ACCESSION      AC073853
VERSION        AC073853.2 GI:9638342
KEYWORDS       HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE          The sequence of Homo sapiens clone
REFERENCE      Unpublished
AUTHORS        2 (bases 1 to 193157)
TITLE          Waterston,R.H.
JOURNAL        Direct Submission
SUBMITTED      (29-JUN-2000) Genome Sequencing Center, Washington
UNIVERSITY     University School of Medicine, 4444 Forest Park Parkway, St. Louis
MO 63108, USA
COMMENT        On Aug 17, 2000 this sequence version replaced gi:8810552.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0763J06
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big_Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 170987 bases at least Q40
Consensus quality: 178667 bases at least Q30
Consensus quality: 182600 bases at least Q20
Insert size: 206000; agarose-fp
Insert size: 190166; sum-of-contigs
Quality coverage: 3.06 in Q20 bases; agarose-fp
Quality coverage: 3.39 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1      1452: contig of 1452 bp in length
*      1453      1552: gap of unknown length
*      1553      3244: contig of 1632 bp in length
*      3245      3344: gap of unknown length
*      3345      4734: contig of 1390 bp in length
*      4735      4834: gap of unknown length
*      4835      6349: contig of 1515 bp in length
*      6350      6449: gap of unknown length
*      6450      8132: contig of 1683 bp in length
*      8133      8232: gap of unknown length
*      8233      10016: contig of 1784 bp in length
*      10017     10116: gap of unknown length
*      10117     12142: contig of 2026 bp in length
*      12143     12242: gap of unknown length
*      12243     13938: contig of 1666 bp in length
*      13939     14038: gap of unknown length
*      14039     15728: contig of 1650 bp in length
*      15729     15828: gap of unknown length
*      15829     18108: contig of 2280 bp in length
*      18109     21376: contig of 3168 bp in length
*      21377     21476: gap of unknown length
*      21477     24103: contig of 2627 bp in length
*      24104     24203: gap of unknown length

```

| | | | | |
|----------|--------------|--------------------------------|--------|------------------------------|
| | * | 24204 | 27825 | contig of 3622 bp in length |
| | * | 27826 | 27825 | gap of unknown length |
| | * | 27926 | 31332 | contig of 3407 bp in length |
| | * | 31333 | 31432 | gap of unknown length |
| | * | 31433 | 36077 | contig of 4645 bp in length |
| | * | 36078 | 36177 | gap of unknown length |
| | * | 36178 | 40497 | contig of 4320 bp in length |
| | * | 40498 | 40597 | gap of unknown length |
| | * | 40598 | 45214 | contig of 4617 bp in length |
| | * | 45215 | 45314 | gap of unknown length |
| | * | 45315 | 50376 | contig of 5062 bp in length |
| | * | 50377 | 50476 | gap of unknown length |
| | * | 50477 | 56846 | contig of 6370 bp in length |
| | * | 56847 | 56946 | gap of unknown length |
| | * | 56947 | 63713 | contig of 6767 bp in length |
| | * | 63714 | 63813 | gap of unknown length |
| | * | 63814 | 70453 | contig of 6640 bp in length |
| | * | 70454 | 70553 | gap of unknown length |
| | * | 70554 | 77281 | contig of 6728 bp in length |
| | * | 77282 | 77381 | gap of unknown length |
| | * | 77382 | 84766 | contig of 7385 bp in length |
| | * | 84767 | 84866 | gap of unknown length |
| | * | 84867 | 91565 | contig of 6699 bp in length |
| | * | 91566 | 91665 | gap of unknown length |
| | * | 91666 | 99088 | contig of 7423 bp in length |
| | * | 99089 | 99188 | gap of unknown length |
| | * | 99189 | 108098 | contig of 8910 bp in length |
| | * | 108099 | 108198 | gap of unknown length |
| | * | 108199 | 114947 | contig of 6749 bp in length |
| | * | 114948 | 115047 | gap of unknown length |
| | * | 115048 | 126524 | contig of 11477 bp in length |
| | * | 126525 | 126624 | gap of unknown length |
| | * | 126625 | 138219 | contig of 11595 bp in length |
| | * | 138220 | 138319 | gap of unknown length |
| | * | 138320 | 152121 | contig of 13802 bp in length |
| | * | 152122 | 152221 | gap of unknown length |
| | * | 152222 | 165974 | contig of 13753 bp in length |
| | * | 165975 | 166074 | gap of unknown length |
| | * | 166075 | 179999 | contig of 13925 bp in length |
| | * | 180000 | 180099 | gap of unknown length |
| | * | 180100 | 193157 | contig of 13058 bp in length |
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| | | /mol_type="genomic DNA" | | |
| | | /db_xref="taxon:9606" | | |
| | | /chromosome="6" | | |
| | | /clone="RP11-763J6" | | |
| | misc_feature | 1..1452 | | |
| | | /note="assembly_name:Contig2" | | |
| | misc_feature | 1553..3244 | | |
| | | /note="assembly_name:Contig9" | | |
| | misc_feature | 3345..4734 | | |
| | | /note="assembly_name:Contig14" | | |
| | misc_feature | 4833..6349 | | |
| | | /note="assembly_name:Contig15" | | |
| | misc_feature | 6450..8132 | | |
| | | /note="assembly_name:Contig16" | | |
| | misc_feature | 8233..10016 | | |
| | | /note="assembly_name:Contig17" | | |
| | misc_feature | 10117..12142 | | |
| | | /note="assembly_name:Contig18" | | |
| | misc_feature | 12243..11938 | | |
| | | /note="assembly_name:Contig19" | | |
| | misc_feature | 14039..15728 | | |
| | | /note="assembly_name:Contig20" | | |
| | misc_feature | 15829..18108 | | |
| | | /note="assembly_name:Contig21" | | |
| | misc_feature | 18209..21376 | | |
| | | /note="assembly_name:Contig22" | | |
| | misc_feature | 21477..24103 | | |
| | | /note="assembly_name:Contig23" | | |
| | misc_feature | 24204..27825 | | |

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misc_feature /note="assembly_name:Contig24"
27926..31332
/note="assembly_name:Contig25"
31433..336077
misc_feature /note="assembly_name:Contig26"
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/note="assembly_name:Contig27"
40598..45214
misc_feature /note="assembly_name:Contig28"
45315..50376
/note="assembly_name:Contig29"
50477..56846
misc_feature /note="assembly_name:Contig30"
56947..63713
/note="assembly_name:Contig31"
63814..70453
misc_feature /note="assembly_name:Contig32"
70554..77281
/note="assembly_name:Contig33"
77382..84766
misc_feature /note="assembly_name:Contig34"
84867..91565
/note="assembly_name:Contig35"
91666..99088
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99189..108098
/note="assembly_name:Contig37"
108199..114947
misc_feature /note="assembly_name:Contig38"
115048..126524
/note="assembly_name:Contig39"
126625..138219
misc_feature /note="assembly_name:Contig40"
138320..152121
/note="assembly_name:Contig41"
clone_end:177
vector_side:left"
misc_feature 152222..165974
/note="assembly_name:Contig42"
166075..179999
/note="assembly_name:Contig43"
clone_end:SP6
vector_side:left"
misc_feature 180100..193157
/note="assembly_name:Contig44"
BASE COUNT 57340 a 37593 c 37870 g 57114 t 3240 others
ORIGIN

Query Match 3.4%; Score 21; DB 2; Length 193157;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 TGATGCATATTTACTTTT 292
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Db 140189 TGATGCCATATTTACTTTT 140209

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RESULT 28
AC091388 194036 bp DNA linear INV 19-APR-2001
DEFINITION Drosophila melanogaster, chromosome 2R, region 44C-44D, BAC clone
AC091388
AC091388 complete sequence.
VERSION AC091388.1 GI:13676915
KEYWORDS HTG.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 194036)
Celisner,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
Holt,R.A., Evans,C.A., Gocayne,J.D., Amanaides,P.G., Brandon,R.C.,

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Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Fartan,D.,
Ferreira,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Pachb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phouanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Swirskas,R., Tector,C., Williams,S.M.,
Zaveri,J.S., Smith,H.O., Rubin,G.M., and Venter,J.C.
Sequencing of Drosophila chromosome 2R, region 44C-44D
Unpublished
2 (bases 1 to 194036)
Celisner,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
Holt,R.A., Evans,C.A., Gocayne,J.D., Amanaides,P.G., Brandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Fartan,D.,
Ferreira,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Pachb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phouanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Swirskas,R., Tector,C., Williams,S.M.,
Zaveri,J.S., Smith,H.O., Rubin,G.M., and Venter,J.C.
Direct Submission
Submitted (19-APR-2001) Berkeley Drosophila Genome Project, MS
64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, US
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome
shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdbp@fruitfly.berkeley.edu.
location/Qualifiers
1..194036
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2R"
/map="44C-44D"
/clone="BACR14B02 (D1257)"
/clone_lib="RP11-98 (Roswell) Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
PBACs3.6)"
BASE COUNT 54625 a 42536 c 42389 g 54486 t
ORIGIN

Query Match 3.4%; Score 21; DB 3; Length 194036;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 AAATTTTACATATATTTA 524
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Db 75645 AAATTTTACATATATTTA 75665

```

RESULT 29
AC009120 195342 bp DNA linear PRI 28-FEB-2001
DEFINITION Homo sapiens chromosome 16 clone RP11-484B3, complete sequence.
AC009120
AC009120.8 GI:13162505
VERSION AC009120.8 GI:13162505
KEYWORDS HTG.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS 1 (bases 1 to 195342)

TITLE DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE Unpublished

AUTHORS 2 (bases 1 to 195342)

TITLE DOE Joint Genome Institute.

REFERENCE Direct Submission

AUTHORS Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

JOURNAL 3 (bases 1 to 195342)

TITLE DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE Direct Submission

AUTHORS Submitted (28-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

JOURNAL On Feb 28, 2001 this sequence version replaced gi:9256141.

COMMENT Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.5% of Sequence;

Estimated Total Number of Errors is 0.6.

STS Content:

SHGC-18227 G19282.

FEATURES

source

1..195342

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="16"

/clone="RP11-484B3"

BASE COUNT 60656 a 41071 c 39465 g 54150 t

ORIGIN

Query Match 3.4%; Score 21; DB 9; Length 195342;

Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 AATATTACTTTTATTGCTGT 299

|||||

38548 AATATTACTTTTATTGCTGT 38568

RESULT 30

AC109217/c 195514 bp DNA linear HTG 06-JUN-2003

LOCUS Mus musculus clone RP23-406P18, *** SEQUENCING IN PROGRESS ***, 2

DEFINITION Ordered pieces.

AC109217

AC109217.6 GI:31442466

HTG; HTGS_PHASE2; HTGS_FULFILL; HTGS_ACTIVEPIN.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 195514)

AUTHORS Birren, B., Nusbaum, C., and Lander, E.

TITLE Mus musculus, clone RP23-406P18

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 195514)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Bara, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, V., Campopiano, A., Chang, J., Chazaro, B., Choquet, Y., Colangelo, M., Collins, S., Collinmore, A., Cook, A., Cooke, P., Dearrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goid, S., Goyette, M., Graham, L., Grand-Pierre, N., Hages, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R., Landers, T., Lehocsky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M.,

McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Minga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Notman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riedack, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M.J., Young, G., Zainoun, J., Zemek, L., Zimmer, A. and Zody, M.

REFERENCE Direct Submission

AUTHORS Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 195514)

TITLE Direct Submission

JOURNAL Submitted (06-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIRB

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L20689

Center clone name: 406_P_18

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 45237: contig of 45237 bp in length

* 45238 45337: gap of 100 bp

* 45338 195514: contig of 150177 bp in length.

FEATURES

source

1..195514

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="RP23-406P18"

/clone.lib="RPCT-23 Female Mouse BAC"

BASE COUNT 62916 a 36822 c 36299 g 59083 t 394 others

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 4,6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 528 AACGCTTACAGTGTGCAGA 548
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 Db 23203 AACGCTTACAGTGTGCAGA 23183

RESULT 31
 AC078957
 LOCUS AC078957 198088 bp DNA linear PRI 15-MAR-2002
 DEFINITION Homo sapiens Xp BAC RP11-339E16 (Roswell Park Cancer Institute
 Human BAC Library) complete sequence.
 AC078957
 VERSION AC078957.16 GI:12600444
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 198088)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooke,S.L., Amaralunge,H.C., Are,J.R., Banks,T., Barbarta,J.,
 Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
 Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
 Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carion,T.F.,
 Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
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 Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
 Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Draper,H.,
 Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
 Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
 Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
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 Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hayes,A.,
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 Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
 Joudon,S., Karlsson,E., Kelly,S., Khan,U., King,L., Kovach,J.,
 Kovar,C., Kratovic,J., Kuresli,A., Landry,N., Leal,B., Lewis,L.C.,
 Lewis,L., Li,U., Li,Z., Lichtarge,O., Lien,C., Liu,J., Liu,W.,
 Louisseg,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
 Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
 Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,
 Meier,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
 Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
 Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokemkwo,S.,
 Ogun,M., Okunolu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
 Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
 Quiles,M., Ren,Y., Rivers,M., Rojas,A., Rojupokan,I., Rolfe,M.,
 Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshbar,N.,
 Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H.,
 Stone,H., Suton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
 Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
 Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
 Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
 Watlington,S., Williams,G., Williams,A., Wleciyk,R., Wooden,S.,
 Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
 and Gibbs R.
 Direct Submision
 Unpublished
 2 (bases 1 to 198088)
 Worley,K.C.
 Direct Submision
 Submitted (13-AUG-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 198088)
 Worley,K.C.
 Direct Submision
 Submitted (01-JAN-2001) Human Genome Sequencing Center, Department

REFERENCE
 AUTHORS Baylor Plaza, Houston, TX 77030, USA
 TITLE 4 (bases 1 to 198088)
 JOURNAL Direct Submision
 Submitted (07-APR-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley,K.C.
 Direct Submision
 Submitted (29-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 6 (bases 1 to 198088)
 Worley,K.C.
 Direct Submision
 Submitted (15-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jan 1, 2001 this sequence version replaced gi:11968348.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
 gc-help@bcm.tmc.edu

COMMENT
 CLONE LENGTH: This sequence does not necessarily represent the
 entire insert of this clone. Overlapping regions of clones are only
 sequenced and submitted once, so the sequence for the remainder of
 the insert may be found in the record for the adjacent clones.
 Overlapping clones are noted at the beginning and end of the
 Features listing.

ANNOTATION OF FEATURES:
 STSs are identified using ePCR (Genome Res. 7:541-550) searches
 of a local database that includes entries from dbSTS, GDB, and
 local mapping efforts.
 Repeats are identified using RepeatMasker (A. Smit and P. Green,
 unpublished.) for Human and Mouse sequences.
 Genes and Region of sequence similarity are identified by BLAST
 (Mnc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
 EST and cDNA sequences. Genes demonstrate at least two exons
 flanked by consensus splice sites that maintained sequence
 continuity across the splice junctions. Sequences that are not
 identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
 standard of double strand coverage with a minimum of 2 clones and 2
 reads with no ambiguities or 2 chemistries with a minimum of 2
 clones and 3 reads with no ambiguities. If the sequence quality for
 a region does not meet this standard, it will be indicated in the
 annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
 standards - estimated error rate less than 1 per 10,000 bases.
 Reports of lowest quality individual bases and measures of base
 quality are listed below. Description of the metrics can be found
 at URL:
<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT
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 /mol_type="genomic DNA"
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 /complement(1..2007)
 /note="overlaps bases 1..2007 of clone AC096506"
 /function="clone overlap"
 1621..1648
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 complement(1890..1938)
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FEATURES
 source
 misc_feature
 repeat_region
 repeat_region

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repeat_region      1939..2155
                    /rpt_family="MER20"
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repeat_region      2630..2651
                    /rpt_family="(TTA)n"
repeat_region      4247..4277
                    /rpt_family="(T)n"
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                    /rpt_family="L2"
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                    /rpt_family="AluO"
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repeat_region      complement(9083..9415)
                    /rpt_family="L1MD2"
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                    /rpt_family="L2"
repeat_region      9956..10227
                    /rpt_family="AluSp"
repeat_region      complement(10636..10797)
                    /rpt_family="L1PA8"
repeat_region      10840..10934
                    /rpt_family="MIR"
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repeat_region      11288..12608
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repeat_region      12745..12819
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repeat_region      complement(13579..14024)
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repeat_region      14277..14370
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repeat_region      complement(14434..14566)
                    /rpt_family="FLAM_A"
repeat_region      complement(14593..14762)
                    /rpt_family="MIR"
repeat_region      16144..16186
                    /rpt_family="(TG)n"
repeat_region      complement(16425..16716)
                    /rpt_family="AluSc"
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Query Match 3.4%; Score 21; DB 9; Length 196088;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 372 TAAATTTAATTAATAAGG 392
DB 183404 TAAATTTAATTAATAAGG 183424

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RESULT 32
AC126275
LOCUS 215435 bp DNA linear HTG 04-JUL-2002
DEFINITION Mus musculus chromosome UNK clone RP23-11N117, WORKING DRAFT
ACCESSION AC126275
VERSION AC126275.1 GI:21694003
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 215435)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
2 (bases 1 to 215435)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (04-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
```

COMMENT

```
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA011N17
----- Summary Statistics -----
Sequencing vector: plasmid, 100%
Chemistry: Dye-primer BT, 0% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 209748 bases at least Q40
Consensus quality: 210894 bases at least Q30
Consensus quality: 211541 bases at least Q20
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1598: contig of 1598 bp in length
* 1599 gap of unknown length
* 3852: contig of 2154 bp in length
* 3853 gap of unknown length
* 3952: contig of 1468 bp in length
* 3953 gap of unknown length
* 5520: contig of 6082 bp in length
* 5521 gap of unknown length
* 11603: contig of 7270 bp in length
* 11603 gap of unknown length
* 11703: contig of 15140 bp in length
* 18973: contig of 6522 bp in length
* 19073: contig of 8682 bp in length
* 25594: contig of 16119 bp in length
* 25595 gap of unknown length
* 34376: contig of 24840 bp in length
* 34477 gap of unknown length
* 45750 gap of unknown length
* 45849: contig of 15140 bp in length
* 60989: gap of unknown length
* 61089: contig of 16018 bp in length
* 71107: contig of 16018 bp in length
* 72108 gap of unknown length
* 72208 contig of 16119 bp in length
* 93326: contig of 16119 bp in length
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* 93426: gap of unknown length
* 118266: contig of 24840 bp in length
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* 118267 118366: gap of unknown length
* 118367 145520: contig of 27154 bp in length
* 145521 145620: gap of unknown length
* 145621 178124: contig of 32504 bp in length
* 178125 178224: gap of unknown length
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Location/Qualifiers

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FEATURES

source

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ORIGIN

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 347 CAAAGCTTTTAATTAAAT 367
DB 139645 CAAAGCTTTTAATTAAAT 139665

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RESULT 33
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LOCUS AB073376
DEFINITION Oryzias latipes DNA, MHC Class I Region, complete cds, section 1/2.
ACCESSION AB073376 BA000027
VERSION AB073376.1 GI:18157518
KEYWORDS
SOURCE
ORGANISM Oryzias latipes (Japanese medaka)
Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Albirostriformes;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE
1 Matsuo, M. Y., Asakawa, S., Shimizu, N., Kimura, H. and Nonaka, M.
Nucleotide sequence of the MHC class I genomic region of a teleost,
the medaka (Oryzias latipes)
JOURNAL Immunogenetics 53 (10-11), 930-940 (2002)

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MEDLINE 21850510
PUBMED 11862394
REFERENCE 2 (bases 1 to 216734)
AUTHORS Watsuo, M. Y., Asakawa, S., Shimizu, N., Kimura, H. and Nonaka, M.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2001) Megumi Y Watsuo, University of Tokyo,
Department of Biological Sciences, Graduate School of Science;
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
(E-mail: megabiol.s.u-tokyo.ac.jp, Tel: 81-3-5841-4064,
Fax: 81-3-5841-4064)

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FEATURES

source

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gene
CDS
LTR
gene
CDS

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Query Match

Best Local Similarity 3.4%; Score 21; DB 5; Length 216734;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 230 ATGCTTATTATTATTTGTTG 250
Db 14691 ATGCTTATTATTATTTGTTG 14671

RESULT 34
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LOCUS Homo sapiens chromosome X clone RP11-607K23, WORKING DRAFT
DEFINITION
SEQUENCE, 19 unordered pieces.
AC021166
AC021166.5 GI:9838294
KEYWORDS
HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE
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ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 218708)
Waterson,R.H.
TITLE
The sequence of Homo sapiens clone
JOURNAL
Unpublished
2 (bases 1 to 218708)
Waterson,R.H.
AUTHORS
Direct Submission
SUBMITTED (14-JUN-2000) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108 USA
On Aug 17, 2000 this sequence version replaced gi:8570350.

COMMENT
Genome Center -----

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Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
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Project Information
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Center project name: H_NH0607K23
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Summary Statistics
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Sequencing vector: M13, 84k
Sequencing vector: Plasmid; 16k
Chemistry: Dye-primer ET; 84k of reads
Chemistry: Dye-terminator Big Dye; 16k of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 205213 bases at least Q40
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Insert size: 219000; agarose-ftp
Insert size: 218241; sum-of-ctigs
Quality coverage: 4.39 in Q20 bases; agarose-ftp
Quality coverage: 4.46 in Q20 bases; sum-of-ctigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 2204: contig of 2204 bp in length
* 2205 2304: gap of unknown length
* 2305 4235: contig of 1931 bp in length
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* 22194 32641: contig of 10448 bp in length
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* 40448 40547: gap of unknown length
* 40548 52107: contig of 11560 bp in length
* 52108 52207: gap of unknown length
* 52208 61381: contig of 9174 bp in length
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* 74337 86944: contig of 12608 bp in length
* 86945 87044: gap of unknown length
* 87045 100053: contig of 13009 bp in length
* 100054 100153: gap of unknown length
* 100154 112917: contig of 12764 bp in length
* 112918 113017: gap of unknown length
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* 126632 126731: gap of unknown length
* 126732 141967: contig of 15236 bp in length
* 141968 142067: gap of unknown length
* 142068 160148: contig of 18081 bp in length
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COMMENT ----- Genome Center

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9**

★ 1 7401: contig of 7401 bp in length

FEATURES

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229 TATGCTTATTATTTATGTT 249

LOCUS

VERSION

ORGANIS

JOURNAL

AUTHORS

• • • • •

РЕЗУЛЬТАТЫ

guerre

```
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between residues 27 and 28
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/db_xref="GI:23505151"
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ILFRLSLRISYCSKGLKYICFLITLISLIEYETNNIPKIDYDEFLKCLFLVRL
FSANLVFLYHLTKVKNIKDEKLNDSDSTQSYAEPTNTTENNHNONNNNNNN
IHNHNHNHNHNHNHNHNNDPCNNHNDPCNNYKQNDPLKSNVTYSHNNLFEEN
IPHVQHTGIIITSKTLPOENIYVLKIVSIPPEKEIINDOTNISHYEMQTDSEFHY
QVNNLSSNNINNDKITPEITTHNLKNNAAYTNHIIQNNHVNYVEHPKGLQYYPG
NHTHNMGNINIC"
gene
join(11425..12434,12559..12655,12774..12908)
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/note="No pfam hit; ScanProsite hit to PS00430; Interpro
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KLNOIKVENIYHOGYKQKQKRNKPNPVSIIIKHKKYFNKONKADICGBAEIART
LDGWYKSFDDIYQNVYVTPCNITQPLNNNSYOCFLISTLMDTWKLLIPESVRL
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complement(13154..14893)
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complement(13154..14893)
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/EC_number="6.1.1.15"
/note="Similarities to prolyl-t-RNA synthetases of bacterial
origin; N-terminal signal peptide. Similar to Lactococcus
lactis prolyl-tRNA synthetase pros or 112127 SMALL:O9CDT4
(EMBL:AB06441) (616 aa) fasta scores: E(): 1.6e-09,
35.21% id in 213 aa, and to Escherichia coli prolyl-tRNA
synthetase pros or drpa or b0194 SMALL:SYF_ECOLI
(SMALL:P16659) (572 aa) fasta scores: E(): 7.3e-08, 31.91%
id in 235 aa. Pfam match to PF00587, tRNA synthetase class
II (G, H, P, S and T)
Signal peptide predicted for PF11240c by SignalP 2.0 HMM
(Signal peptide probability 0.720, signal anchor
probability 0.018) with cleavage site probability 0.591
between residues 18 and 19"
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NDKSEBSLKKKIEDDGYILSPCESSLSLINOYNNITIKCLPLIHOVYKERN
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1.9e-180, 99.14% id in 466 aa. Pfam match to PF00149,
Ser/Thr protein phosphatase; SMART hit to SM00156, Protein
phosphatase 2A homologues, catalytic domain."
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VDEMTCKLIKKEIKLEBKVMCDLLIILKNBECAVINVTVAAGIHQGFPLD
LPHIGLSPDVNVIYFLGPYVGRYSCGFCVACFKIYSGRVATLLAGNHSRQITK
YVGFDECKIRKNNNIYWKITUDYFDYFLPITAIINDEIFCDHGASISPLQITDEINK
LDRFEIYQDAGIICDLWSDPAGPDEDLTEGKPSRAGVIFSEKESFLRNKLIS
CIRAHQLVQDGFQWMHNDKVVYTFSAENYCCRCNCASLMLVDFEMEDFTTFVTAP
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20291..20343)
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 18957 GFMATGCTTATTATTAT 18977

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RESULT 37
LOCUS AE003827
DEFINITION Drosophila melanogaster chromosome 2R, section 23 of 74 of the complete sequence.
ACCESSION AE003827 AE013599
VERSION AE003827.3 GI:21627498
KEYWORDS
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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AUTHORS
1 (bases 1 to 256227)
Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X., Brandon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfeiffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gaber,G.L., Abail,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Balabin,D., Ballew,R.M., Basu,A., Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y., Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S., Borokov,D., Botchan,M.R., Bock,J., Brokstein,P., Brotter,P., Burris,K.C., Busam,D.A., Butler,H., Cadeau,E., Center,A., Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferrara,S., Ferrieres,S., Fleischmann,W., Foster,C., Gabrielian,A.E., Garz,C., Gelbart,W.M., Glasser,K., Glodek,A., Gong,P., Gorrell,J.H., Gu,Z., Guan,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J., Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J., Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z., Kemison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C., Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A., Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Matesi,B., McIntosh,T.C., McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C., Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L., Murthy,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K., Nusken,D.R., Pacle,J.M., Palazolo,M., Peltman,G.S., Pan,S., Pollard,J., Puri,V., Reese,M.G., Reiner,K., Remington,K., Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I., Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C., Stapleton,M., Strong,R., Sun,E., Svitek,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A., Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodruff,Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of *Drosophila melanogaster*
Science 287 (5461), 2185-2195 (2000)
20196006
10731132

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2 (bases 1 to 256227)
Celniker,S.E., Adams,M.D., Krommiller,B., Wan,K.H., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y., Barton,J., An,H., Baldwin,D., Barton,J., Beeson,K.Y., Busam,D.A., Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M., Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Fairlan,D., Fertler,S., Frise,E., Galle,R.F., Gary,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Matesi,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunco,J., Phouaneavong,S., Peltman,G.S., Puri,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svitek,R., Tector,C., Tyler,D., Williams,S.M., Zaveri,J.S., Smith,H.O., Venter,J.C. and Rubin,G.M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Sequencing of *Drosophila melanogaster* genome
Unpublished
3 (bases 1 to 256227)
Matera,S., Crosby,M.A., Matthews,B.B., Bayraktaroglu,L., Campbell,K., Hradecky,P., Huang,Y., Kaminker,J.S., Prochnik,S.E., Smith,C.D., Tupy,J.L., Bergman,C.W., Berman,B.P., Carlson,D.W., Celniker,S.E., Clamp,M.E., Drysdale,R.A., Emmert,D., Frise,E., de Grey,A.D.N.J., Harris,N.L., Krommiller,B., Marshall,B., Millburn,G.H., Richter,J., Russo,S., Seale,S.M.J., Smith,E., Shu,S., Smutniak,F., Whitfield,E.J., Ashburner,M., Gelbart,W.M., Rubin,G.M., Mungall,C.J. and Lewis,S.E.
Annotation of *Drosophila melanogaster* genome
Unpublished
4 (bases 1 to 256227)
Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
JOURNAL
TITLE
REFERENCE
AUTHORS

Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
5 (bases 1 to 256227)
FlyBase
Direct Submission
JOURNAL
TITLE
REFERENCE
AUTHORS

Submitted (06-SEP-2002) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 256227)
FlyBase
Direct Submission
JOURNAL
TITLE
REFERENCE
AUTHORS

Submitted (23-JUN-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
On Jun 28, 2002 this sequence version replaced gi:10727648.
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/db_xref="taxon:7227"
/chromosome="2R"
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CDS
mRNA
gene
mRNA

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    KILKSIQILPERSNLTWMIILPTAIDGLPLEEKLGLDNKEVAKSIKMEVYTI
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 38
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DEFINITION Homo sapiens Chromosome 16 BAC clone CIT9878K-A-248F7, complete
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ACCESSION AC004605
VERSION AC004605.1 GI:3337395
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
    1 (bases 1 to 259474)
    Lotfus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R.,
    Fuhrman,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,
    Deslattes Mays,A., Cao,Y., Xu,R.X., Kerlavage,A.R. and Venter,J.C.
    Eichler,B.B., Harris,P.C., Venter,J.C. and Adams,M.D.
    Genome duplications and other features in 12 Mb of DNA sequence
    from human chromosome 16p and 16q
    Genomics 60 (3), 295-308 (1999)
JOURNAL
    MEDLINE 99425270
    PUBMED 10493829
REFERENCE
    2 (bases 1 to 259474)
    Adams,M.D., Lotfus,B.J., Zhou,L., Crosby,M., Fuhrmann,J.,
    Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
    Homo sapiens Chromosome 16 BAC clone CIT9878K-A-248F7
    Unpublished
    3 (bases 1 to 259474)
    Adams,M.D. and Lotfus,B.J.
    Direct Submission
    Submitted (23-APR-1998) The Institute for Genomic Research, 9712
    Medical Center Dr, Rockville, MD 20850, USA, Email:
    b.jlotfus@igrr.org
    4 (bases 1 to 259474)
    Adams,M.D. and Lotfus,B.J.
    Direct Submission
    Submitted (24-JUL-1998) The Institute for Genomic Research, 9712
    Medical Center Dr., Rockville, MD 20850, USA
    On Jul 24, 1998 this sequence version replaced gi:3228501.
    Address all correspondence to: Mark Adams The Institute for Genomic
    Research 9712 Medical Center Dr, Rockville, MD 20850, USA e-mail
    address: humen@igrr.org. The orientation of the sequence is from
    SP6 end to T7 end. Genes were identified by a combination of five
    methods including: XGRAIL (available by anonymous ftp from
    arthur.epm.ornl.gov), GeneFinder (Phil Green, University of
    Washington), Genscan (Chris Burge,
    http://genomic.stanford.edu/~chris/GENSCANW.html) searches of the
    complete sequence against a peptide database and the Human gene
    index database at TRIGR (http://www.tigr.org/tcd/ngi.html).
    Genes without peptide homology having spliced EST hits are termed
    'Unknown gene product'. Genes encoding tRNAs are predicted by
    tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
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    /db_xref="dbSTS:G02122"
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    /note="32826, A002D07, Chr. -, Homo sapiens"
    /db_xref="dbSTS:G19348"
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    ORIGIN

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| Query Match | 3.4%; | Score 21; | DB 9; | Length 259474; | |
| Best Local Similarity | 100.0%; | Pred. NO. 4.6; | | | |
| Matches 21; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; | |
| QY | 279 | AATATTACTTTTATGCTGT | 299 | | |
| DB | 37466 | AATATTACTTTTATGCTGT | 37446 | | |
| RESULT 39 | | | | | |
| AE003837 | | | | | |
| LOCUS | 265215 bp | DNA | linear | INV 14-FEB-2003 | |
| DEFINITION | Drosophila melanogaster chromosome 2R, section 13 of 74 of the complete sequence. | | | | |
| ACCESSION | AE003837 | AE003837 | | | |
| VERSION | AE003837.3 | GI:21627669 | | | |
| KEYWORDS | | | | | |
| SOURCE | | | | | |
| ORGANISM | Drosophila melanogaster (fruit fly) | | | | |
| REFERENCE | Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yeates,M.D., Zhang,Q., Chen,L.X., Brannon,R.C., Rogers,Y.H., Blazer,R.G., Chame,M., Pfeiffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabot,G.L., Abell,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Baldwin,D., Ballew,R.M., Basu,A., Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y., Benos,P.V., Bernier,B.P., Bhandari,D., Bolshakov,S., Borkov,C., Botchan,M.R., Bouck,U., Brockstein,P., Brotter,P., Burris,K.C., Busam,D.A., Butler,H., Cadieu,E., Center,A., Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C., Ferreira,S., Fleischmann,W., Foster,C., Gabrielian,A.E., Garay,N.S., Gehart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z., Guan,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J., Hernandez,J.R., Houck,U., Hostin,D., Houston,K.A., Howland,T.J., Wei,M.H., Ibegwam,C., Jalali,M., Kalish,F., Karpén,G.H., Ke,Z., Kienlen-Da,A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C., Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A., Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Liu,X., Mattei,B., McIntosh,T.C., McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C., Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L., Murthy,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K., Nusser,D.R., Pacleb,J.M., Palazolo,M., Peltman,G.S., Pan,S., Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K., Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I., Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spreading,A.C., Stepieton,M., Strong,R., Sun,E., Switzkas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A., Weinstock,G.M., Weisenbach,J., Williams,S.M., Woodage,T., Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,D., Yeh,R.F., Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C. | | | | |
| TITLE | The genome sequence of Drosophila melanogaster | | | | |
| JOURNAL | Science 287 (5461), 2185-2195 (2000) | | | | |
| MEDLINE | 20196006 | | | | |
| REFERENCE | 10731132 | | | | |
| AUTHORS | 2 (bases 1 to 265215) | | | | |
| | Celniker,S.E., Adams,M.D., Krommiller,B., Wan,K.H., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y., Bannan,J., An,H., Baldwin,D., Bannan,J., Beeson,K.Y., Busam,D.A., Carlson,J.W., Center,A., Chame,M., Davenport,L.B., Dietz,S.M., Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Fartan,D., Ferreira,S., Frise,E., Galle,R.F., Gary,N.S., George,R.A., Gonzalez,M., Houck,U., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Matcel,B., Moshrefi,A., | | | | |

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|--|-------------------------|--|---------|---------|
| TITLE | JOURNAL | REFERENCE | AUTHORS | COMMENT |
| 3 (bases 1 to 265215) | Unpublished | | | |
| McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Pacle,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanavong,S., Peltman,G.S., Puri,V., Richards,S., Scheeler,F., Stepieton,M., Strong,R., Switzkas,R., Tector,C., Tyler,D., Williams,S.M., Zaveri,J.S., Smith,H.O., Venter,J.C. and Rubin,G.M. | | | | |
| Sequencing of Drosophila melanogaster genome | | | | |
| REFERENCE | | | | |
| 4 (bases 1 to 265215) | Unpublished | | | |
| Miera,S., Crosby,M.A., Matthews,B.B., Bayraktaroglu,L., Campbell,K., Hradecky,P., Huang,Y., Kaminker,J.S., Prochnik,S.E., Smith,C.D., Tupy,J.L., Bergman,C.M., Bertman,B.P., Carlson,J.W., Celniker,S.E., Clamp,M.E., Drysdale,R.A., Emmert,D., Frise,E., de Grey,A.D.N.J., Harris,N.L., Krommiller,B., Marshall,B., Millburn,G.H., Richter,J., Russo,S., Seale,S.M.J., Smith,E., Shu,S., Smutniak,F., Whitfield,E.J., Ashburner,M., Gelbart,W.M., Rubin,G.M., Mungall,C.J. and Lewis,S.E. | | | | |
| Annotation of Drosophila melanogaster genome | | | | |
| REFERENCE | | | | |
| 5 (bases 1 to 265215) | Submitted (21-MAR-2000) | Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA | | |
| REFERENCE | | | | |
| 6 (bases 1 to 265215) | Submitted (06-SEP-2002) | University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA | | |
| REFERENCE | | | | |
| 7 (bases 1 to 265215) | Submitted (23-JUN-2003) | University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA | | |
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| | |
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| RESULT 40 | |
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| DEFINITION | Drosophila melanogaster ribosomal RNA large subunit ribosomal RNA (m1:rRNA) gene, partial sequence; and unknown gene; mitochondrial genes for mitochondrial products. |
| ACCESSION | J01409 |
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| SEGMENT | 2 of 2 |
| SOURCE | mitochondrion Drosophila melanogaster (fruit fly) |
| ORGANISM | Drosophila melanogaster |
| REFERENCE | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 172) Clarry,D.O., Goddard,J.M., Martin,S.C., Fauron,C.M. and Wolstenholme,D.R. Drosophila mitochondrial DNA: a novel gene order Nucleic Acids Res. 10 (21), 6619-6637 (1982) |
| AUTHORS | |
| TITLE | |
| JOURNAL | |
| MEDLINE | 83090428 |
| PUBMED | 6294611 |
| REFERENCE | |
| AUTHORS | |
| TITLE | 2 (bases 1 to 172) de Bruijn,M.H. Drosophila melanogaster mitochondrial DNA, a novel organization and genetic code |
| JOURNAL | Nature 304 (5923), 234-241 (1983) |
| MEDLINE | 83245048 |
| PUBMED | 6408489 |
| COMMENT | Compared with mouse, human, and bovine mitochondrial genomes. The |

Compared with mouse, human, and bovine mitochondrial genomes. The order of genes is different in *Drosophila* and mammalian mitochondria. Corresponding genes also appear on different strands. The codon 'aga' codes for arginine in *Drosophila* and is not present or is a termination codon in the mammals. 'tga' codes for tryptophan rather than termination. Origin of replication is located within the 'at' rich region approx 250-450 bp from the 5' boundary. The 'at' rich region varies in size between strains and species of *Drosophila* and does not appear to be transcribed. The direction of replication is in the same direction as transcription of all genes in this segment.

| FEATURES | SOURCE |
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| ORIGIN | |

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| Best Local Similarity | 100.0% | Pred. No. 19 | | |
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Wed Oct 8 12:17:09 2003

us-10-010-160-1.oligo.rge

Page 45

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| C 137 | 17 | 2.7 | 618 | 24 | ABO30469 | Oligonucleotide fo |
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| C 147 | 17 | 2.7 | 776 | 22 | AAH05122 | Human ovarian anti |
| C 148 | 17 | 2.7 | 802 | 22 | AAH29469 | Drosophila melanog |
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| 230 | 17 | 2.7 | 6069 | 24 | ABL70440 | Chemically treated | 303 | 16 | 2.6 | 235 | 21 | AAA1853 | Human secreted exp |
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| 232 | 17 | 2.7 | 6069 | 24 | ABK31467 | Signal transductio | c 305 | 16 | 2.6 | 251 | 19 | AAK11661 | Human biallelic po |
| 233 | 17 | 2.7 | 6096 | 24 | ABK92513 | Human prostate spe | c 306 | 16 | 2.6 | 251 | 19 | AAK12829 | Human biallelic po |
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| C 238 | 17 | 2.7 | 6531 | 24 | ABL32640 | Human immune syste | 311 | 16 | 2.6 | 292 | 24 | ABL83926 | Human ovarian canc |
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| C 243 | 17 | 2.7 | 6929 | 24 | ABL34158 | Human immune syste | c 316 | 16 | 2.6 | 318 | 22 | AA180375 | Human polynucleoti |
| C 244 | 17 | 2.7 | 7321 | 24 | ABL70386 | Chemically treated | c 317 | 16 | 2.6 | 321 | 13 | AAQ26718 | Encodes exon VI of |
| C 245 | 17 | 2.7 | 7321 | 24 | AAS61338 | Human gene regulat | c 318 | 16 | 2.6 | 330 | 16 | AAI25130 | Human gene signatu |
| C 246 | 17 | 2.7 | 7321 | 24 | ABK31425 | Signal transductio | c 319 | 16 | 2.6 | 337 | 22 | AA512430 | DNA encoding 1-amt |
| C 247 | 17 | 2.7 | 7573 | 18 | AAI58681 | DNA encoding human | c 320 | 16 | 2.6 | 352 | 24 | ABQ97063 | Mouse ES cell rela |
| C 248 | 17 | 2.7 | 7573 | 18 | ABK83875 | Human cDNA differe | c 321 | 16 | 2.6 | 375 | 22 | AAK78834 | Human immune/haema |
| C 249 | 17 | 2.7 | 7573 | 24 | ABN95697 | Gene #1295 used to | c 322 | 16 | 2.6 | 391 | 22 | AAK75457 | Human immune/haema |
| C 250 | 17 | 2.7 | 7849 | 24 | ABL92279 | Chemically treated | 323 | 16 | 2.6 | 396 | 22 | ABA70405 | Human foetal liver |
| C 251 | 17 | 2.7 | 7849 | 24 | AAD22330 | Chemically treated | 324 | 16 | 2.6 | 396 | 22 | ABA57065 | Probe #1531 for g |
| C 252 | 17 | 2.7 | 7900 | 22 | AAS46759 | Tumour suppressor | 325 | 16 | 2.6 | 396 | 22 | AAK18645 | Human brain expres |
| C 253 | 17 | 2.7 | 9032 | 22 | ABL18256 | Drosophila melanog | 326 | 16 | 2.6 | 396 | 22 | AAK44573 | Human bone marrow |
| C 254 | 17 | 2.7 | 9110 | 24 | ABL34429 | Drosophila melanog | 327 | 16 | 2.6 | 396 | 22 | AAI24923 | Probe #14856 for g |
| C 255 | 17 | 2.7 | 9667 | 23 | ABL19960 | Human immune syste | 328 | 16 | 2.6 | 396 | 22 | AAI50556 | Probe #19242 used |
| C 256 | 17 | 2.7 | 10183 | 22 | AAS46752 | Drosophila melanog | 329 | 16 | 2.6 | 396 | 22 | AB544231 | Human liver single |
| C 257 | 17 | 2.7 | 11046 | 24 | ABK31537 | Signal transductio | 330 | 16 | 2.6 | 396 | 24 | AB518810 | Human genome-deriv |
| C 258 | 17 | 2.7 | 13784 | 24 | ABK40061 | Human chemically p | c 331 | 16 | 2.6 | 398 | 22 | AAI92252 | Human polynucleoti |
| C 259 | 17 | 2.7 | 14847 | 23 | ABL02458 | Drosophila melanog | c 332 | 16 | 2.6 | 402 | 23 | ABV13541 | Human prostate exp |
| C 260 | 17 | 2.7 | 15817 | 23 | ABL08312 | Drosophila melanog | c 333 | 16 | 2.6 | 410 | 25 | ABK54088 | Bovine EST associa |
| C 261 | 17 | 2.7 | 17211 | 24 | ABL32654 | Human immune syste | c 334 | 16 | 2.6 | 419 | 22 | AAI87346 | Human polynucleoti |
| C 262 | 17 | 2.7 | 21747 | 23 | ABL09060 | Drosophila melanog | c 335 | 16 | 2.6 | 420 | 23 | ABV15141 | Human prostate exp |
| C 263 | 17 | 2.7 | 23109 | 22 | AAK82298 | Human immune/haema | 336 | 16 | 2.6 | 423 | 22 | AAK78273 | Human immune/haema |
| C 264 | 17 | 2.7 | 24259 | 22 | AAS46691 | Tumour suppressor | 337 | 16 | 2.6 | 424 | 20 | AAK21122 | Human immune/haema |
| C 265 | 17 | 2.7 | 24401 | 23 | ABL03396 | Drosophila melanog | c 338 | 16 | 2.6 | 430 | 25 | ABK54123 | Polynucleotide seq |
| C 266 | 17 | 2.7 | 28470 | 22 | AAK71445 | Human immune/haema | 339 | 16 | 2.6 | 435 | 22 | AAK59495 | Bovine EST associa |
| C 267 | 17 | 2.7 | 28482 | 25 | ABZ73855 | Secreted protein g | c 340 | 16 | 2.6 | 441 | 25 | ABK54060 | Bovine EST associa |
| C 268 | 17 | 2.7 | 32681 | 25 | ABZ73854 | Secreted protein g | c 341 | 16 | 2.6 | 445 | 22 | ABAI6413 | Human nervous syst |
| C 269 | 17 | 2.7 | 32681 | 25 | ABZ74517 | Secreted protein g | c 342 | 16 | 2.6 | 451 | 21 | AAK37054 | Arabidopsis thalia |
| C 270 | 17 | 2.7 | 32681 | 25 | ABZ68053 | Human secreted pro | c 343 | 16 | 2.6 | 457 | 21 | AAK66002 | Human lung cancer |
| C 271 | 17 | 2.7 | 47108 | 24 | ABK31510 | Signal transductio | c 344 | 16 | 2.6 | 457 | 24 | ABO92407 | Human lung cancer |
| C 272 | 17 | 2.7 | 80578 | 22 | AAH44800 | Human GPCR protein | c 345 | 16 | 2.6 | 457 | 24 | ABL49221 | Human polynucleoti |
| C 273 | 17 | 2.7 | 90220 | 24 | ABK83576 | Human cDNA differe | c 346 | 16 | 2.6 | 462 | 22 | ABA20650 | Human nervous syst |
| C 274 | 17 | 2.7 | 90541 | 24 | ABSS52847 | Human SR protein-s | c 347 | 16 | 2.6 | 462 | 22 | AA541700 | Genomic sequence # |
| C 275 | 17 | 2.7 | 92638 | 24 | ABQ08096 | Human osteoblast d | 348 | 16 | 2.6 | 470 | 22 | ABA42791 | Human breast cell |
| C 276 | 17 | 2.7 | 95500 | 24 | AAD41740 | Human RECQL2 DNA # | 349 | 16 | 2.6 | 470 | 22 | ABA53219 | Human foetal liver |
| C 277 | 17 | 2.7 | 100000 | 24 | ABO74541 | Human transglutami | 350 | 16 | 2.6 | 470 | 22 | ABA22994 | Probe #1460 for ge |
| C 278 | 17 | 2.7 | 107820 | 22 | ABD16230 | Human ATP-binding | 351 | 16 | 2.6 | 470 | 22 | AAK01467 | Human brain expres |
| C 279 | 17 | 2.7 | 113033 | 25 | AAI54213 | SR protein-specific | 352 | 16 | 2.6 | 470 | 22 | AAK26915 | Human bone marrow |
| C 280 | 17 | 2.7 | 130480 | 22 | AAI25833 | R. marinus bacteri | 353 | 16 | 2.6 | 470 | 22 | AAI11537 | Probe #1470 for ge |
| C 281 | 17 | 2.7 | 147708 | 24 | ABQ08154 | Human osteoblast d | 354 | 16 | 2.6 | 470 | 22 | AAI12819 | Probe #1505 used t |
| C 282 | 17 | 2.7 | 150905 | 25 | ABZ80818 | Human PAT-2 polymo | 355 | 16 | 2.6 | 470 | 22 | AAI01455 | Probe #1446 used t |
| C 283 | 17 | 2.7 | 349980 | 22 | AAI86431 | Pyrococcus abyssi | 356 | 16 | 2.6 | 470 | 23 | AB526504 | Human liver single |
| C 284 | 17 | 2.7 | 349980 | 22 | AAI86431 | C glutaminc codin | 357 | 16 | 2.6 | 470 | 24 | AB501513 | Human genome-deriv |
| C 285 | 17 | 2.7 | 659158 | 25 | ABX16390 | Mouse high growth | c 358 | 16 | 2.6 | 475 | 22 | AAI16356 | Human polynucleoti |
| C 286 | 17 | 2.7 | 1038602 | 20 | AAZ01425 | Complete genome se | 359 | 16 | 2.6 | 477 | 23 | AA567787 | DNA encoding novel |
| C 287 | 17 | 2.7 | 1691080 | 24 | ABX08036 | Human phosphodiester | 360 | 16 | 2.6 | 480 | 21 | AAAC0685 | Human secreted pro |
| C 288 | 17 | 2.7 | 1830121 | 17 | AAI420063 | Haemophilus influe | 361 | 16 | 2.6 | 482 | 24 | ABK62674 | Rat sequence diffe |
| C 289 | 17 | 2.7 | 2155561 | 24 | ABN71527 | Streptococcus poly | 362 | 16 | 2.6 | 488 | 22 | AAK07395 | Human brain expres |
| C 290 | 17 | 2.7 | 2163598 | 25 | AB556454 | Streptococcus pneu | 363 | 16 | 2.6 | 488 | 22 | AAK33171 | Human bone marrow |
| C 291 | 16 | 2.6 | 44 | 22 | AAD08544 | Vaccinia virus (VV | 364 | 16 | 2.6 | 488 | 22 | AAI18969 | Probe #7655 used t |
| C 292 | 16 | 2.6 | 50 | 24 | ABZ02185 | Human leukocyte ge | 365 | 16 | 2.6 | 488 | 22 | AB532916 | Human liver single |
| C 293 | 16 | 2.6 | 50 | 24 | AAD22237 | Vaccinia virus p11 | 366 | 16 | 2.6 | 488 | 24 | AB507996 | Human genome-deriv |
| C 294 | 16 | 2.6 | 51 | 22 | AAI18734 | Human silent SNP c | 367 | 16 | 2.6 | 490 | 20 | AA532438 | Human cDNA encodin |
| C 295 | 16 | 2.6 | 51 | 22 | AAI18735 | Human silent SNP c | 368 | 16 | 2.6 | 493 | 20 | AAI13759 | Enterococcus faeca |
| C 296 | 16 | 2.6 | 65 | 24 | ABN52782 | Mouse spliced tran | 369 | 16 | 2.6 | 493 | 25 | AB599554 | Enterococcus faeca |
| C 297 | 16 | 2.6 | 111 | 24 | AAD22235 | Vaccinia virus p11 | 370 | 16 | 2.6 | 493 | 25 | ABZ52472 | Aeperyllus oryzae |
| C 298 | 16 | 2.6 | 140 | 22 | AAK24374 | Human brain expres | c 371 | 16 | 2.6 | 496 | 21 | AAK13173 | Plant microsatelli |
| C 299 | 16 | 2.6 | 140 | 22 | AAI56365 | Probe #25051 used | 372 | 16 | 2.6 | 496 | 22 | ABA57789 | Human foetal liver |
| C 300 | 16 | 2.6 | 155 | 21 | AAI22030 | Human breast and o | 373 | 16 | 2.6 | 496 | 22 | ABA27150 | Probe #5616 for ge |

| | | | | | | | | | | | | | |
|-------|----|-----|-----|----|----------|--------------------|-------|----|-----|------|----|-----------|--------------------------|
| 374 | 16 | 2.6 | 496 | 22 | AAK05858 | Human brain expres | C 447 | 16 | 2.6 | 640 | 22 | AAI62984 | Human kidney relat |
| 375 | 16 | 2.6 | 496 | 22 | AAK1492 | Human bone marrow | C 448 | 16 | 2.6 | 642 | 22 | AAK30770 | Human cDNA encodin |
| 376 | 16 | 2.6 | 496 | 22 | AAI15699 | Probe #5632 for ge | C 449 | 16 | 2.6 | 642 | 22 | ABZ51977 | Aspergillus oryzae |
| 377 | 16 | 2.6 | 496 | 22 | AAI37374 | Probe #6060 used t | C 450 | 16 | 2.6 | 656 | 22 | AAI06053 | Human reproductive |
| 378 | 16 | 2.6 | 496 | 23 | ABK31174 | Human liver single | C 451 | 16 | 2.6 | 656 | 23 | ABL98618 | Human testicular a |
| 379 | 16 | 2.6 | 496 | 23 | ABK31174 | Human prostate exp | C 452 | 16 | 2.6 | 660 | 24 | ABO55999 | Human ovarian anti |
| C 380 | 16 | 2.6 | 496 | 24 | ABK06246 | Human genome-deriv | C 453 | 16 | 2.6 | 666 | 22 | AAK91553 | Human cDNA 5'-end |
| C 381 | 16 | 2.6 | 503 | 23 | ABV02224 | Human prostate exp | C 454 | 16 | 2.6 | 666 | 22 | AAK93123 | Human cDNA clone r |
| C 382 | 16 | 2.6 | 504 | 24 | ABO32850 | Oligonucleotide fo | C 455 | 16 | 2.6 | 696 | 24 | ABN92707 | Staphylococcus epi |
| C 383 | 16 | 2.6 | 504 | 24 | ABO32851 | Oligonucleotide fo | C 456 | 16 | 2.6 | 700 | 22 | AAH70572 | Human cervical can |
| C 384 | 16 | 2.6 | 505 | 20 | AAV99730 | Human foetal brain | C 457 | 16 | 2.6 | 704 | 21 | AAAC43752 | Oligonucleotide fo |
| C 385 | 16 | 2.6 | 513 | 21 | AA43861 | Human secreted exp | C 458 | 16 | 2.6 | 707 | 24 | ABO41062 | Oligonucleotide fo |
| C 386 | 16 | 2.6 | 523 | 21 | ABV51773 | Human prostate exp | C 459 | 16 | 2.6 | 707 | 24 | ABO41063 | Oligonucleotide fo |
| C 387 | 16 | 2.6 | 525 | 24 | ABK78696 | Bacillus clausii g | C 460 | 16 | 2.6 | 709 | 22 | AAK34039 | Human cDNA encodin |
| C 388 | 16 | 2.6 | 527 | 23 | ABV32538 | Human prostate exp | C 461 | 16 | 2.6 | 723 | 22 | AAH71575 | Human cDNA encodin |
| C 389 | 16 | 2.6 | 527 | 23 | ABV41463 | Human prostate exp | C 462 | 16 | 2.6 | 736 | 24 | AAAD28990 | Human cervical can |
| C 390 | 16 | 2.6 | 532 | 24 | ABO14879 | Oligonucleotide fo | C 463 | 16 | 2.6 | 738 | 21 | AAA02249 | Human colon cancer |
| C 391 | 16 | 2.6 | 532 | 24 | ABO14879 | Oligonucleotide fo | C 464 | 16 | 2.6 | 739 | 22 | AAAF26890 | Beet necrotic yell |
| C 392 | 16 | 2.6 | 533 | 23 | ABV23852 | Human prostate exp | C 465 | 16 | 2.6 | 746 | 22 | AAAF26891 | Beet necrotic yell |
| C 393 | 16 | 2.6 | 533 | 23 | ABV29729 | Human prostate exp | C 466 | 16 | 2.6 | 746 | 22 | AAAF26891 | Beet necrotic yell |
| C 394 | 16 | 2.6 | 533 | 24 | ABO33248 | Oligonucleotide fo | C 467 | 16 | 2.6 | 754 | 24 | AAH06667 | Human cDNA clone (|
| C 395 | 16 | 2.6 | 533 | 24 | ABO33249 | Oligonucleotide fo | C 468 | 16 | 2.6 | 754 | 24 | ABO22136 | Oligonucleotide fo |
| C 396 | 16 | 2.6 | 535 | 22 | AAI19863 | Human breast cance | C 469 | 16 | 2.6 | 754 | 24 | ABO22136 | Oligonucleotide fo |
| C 397 | 16 | 2.6 | 537 | 22 | AAH11416 | Human CDNA clone (| C 470 | 16 | 2.6 | 793 | 18 | AAV04161 | Phytophthora caps |
| C 398 | 16 | 2.6 | 538 | 23 | ABV52021 | Human prostate exp | C 471 | 16 | 2.6 | 796 | 21 | AACT5469 | Human ORFX ORF1024 |
| C 399 | 16 | 2.6 | 543 | 22 | AAH17171 | Human cervical can | C 472 | 16 | 2.6 | 822 | 22 | AAI95351 | Human neuroblastom |
| C 400 | 16 | 2.6 | 545 | 22 | AAH11494 | Human CDNA clone (| C 473 | 16 | 2.6 | 841 | 22 | AAH06636 | Human cDNA clone (|
| C 401 | 16 | 2.6 | 549 | 24 | ABK53587 | Human eosinophil-m | C 474 | 16 | 2.6 | 846 | 24 | AAK97172 | Human metalloprote |
| C 402 | 16 | 2.6 | 551 | 22 | AAI86614 | Human poly nucleot | C 475 | 16 | 2.6 | 857 | 24 | ABO29998 | Oligonucleotide fo |
| C 403 | 16 | 2.6 | 560 | 22 | AAH06039 | Human CDNA clone (| C 476 | 16 | 2.6 | 857 | 24 | ABO29998 | Oligonucleotide fo |
| C 404 | 16 | 2.6 | 565 | 23 | ABV55407 | Human prostate exp | C 477 | 16 | 2.6 | 873 | 13 | AAQ23662 | Oligonucleotide fo |
| C 405 | 16 | 2.6 | 568 | 22 | ABK63359 | Human foetal liver | C 478 | 16 | 2.6 | 873 | 14 | AAQ23613 | Truncated hepatocy |
| C 406 | 16 | 2.6 | 568 | 22 | ABK05653 | Probe #9029 for ge | C 479 | 16 | 2.6 | 873 | 18 | AAAT78409 | cDNA encoding 34kD |
| C 407 | 16 | 2.6 | 568 | 22 | AAK18999 | Human brain expres | C 480 | 16 | 2.6 | 874 | 20 | AAK01054 | 34 kilodalton hepa |
| C 408 | 16 | 2.6 | 568 | 22 | AAK37602 | Human bone marrow | C 481 | 16 | 2.6 | 913 | 22 | AAI23181 | Nucleotide sequenc |
| C 409 | 16 | 2.6 | 568 | 22 | AAI18357 | Probe #8290 for ge | C 482 | 16 | 2.6 | 917 | 24 | ABO15930 | Human breast cance |
| C 410 | 16 | 2.6 | 568 | 22 | AAI43472 | Probe #12158 used | C 483 | 16 | 2.6 | 917 | 24 | ABO15931 | Oligonucleotide fo |
| C 411 | 16 | 2.6 | 568 | 23 | ABK37258 | Human liver single | C 484 | 16 | 2.6 | 927 | 22 | AAI98932 | Oligonucleotide fo |
| C 412 | 16 | 2.6 | 572 | 24 | ABK11587 | Human genome-deriv | C 485 | 16 | 2.6 | 927 | 22 | AAI63282 | Human kidney relat |
| C 413 | 16 | 2.6 | 576 | 24 | ABK64175 | Toxicologically re | C 486 | 16 | 2.6 | 929 | 24 | ABK6416 | DNA encoding soybe |
| C 414 | 16 | 2.6 | 576 | 24 | ABK64175 | Human cancer relat | C 487 | 16 | 2.6 | 937 | 23 | ABV22590 | DNA encoding soybe |
| C 415 | 16 | 2.6 | 578 | 22 | ABK31471 | Human foetal liver | C 488 | 16 | 2.6 | 937 | 23 | ABV22590 | Human prostate exp |
| C 416 | 16 | 2.6 | 578 | 22 | ABK12797 | Probe #9937 for ge | C 489 | 16 | 2.6 | 962 | 24 | ABK63418 | DNA encoding soybe |
| C 417 | 16 | 2.6 | 578 | 22 | AAK38523 | Human brain expres | C 490 | 16 | 2.6 | 979 | 24 | ABL89923 | Human polynucleoti |
| C 418 | 16 | 2.6 | 578 | 22 | AAK38523 | Human bone marrow | C 491 | 16 | 2.6 | 980 | 24 | ABK63417 | DNA encoding soybe |
| C 419 | 16 | 2.6 | 578 | 22 | AAI19322 | Probe #9255 for ge | C 492 | 16 | 2.6 | 997 | 22 | AAI71907 | Human dthylatoxola |
| C 420 | 16 | 2.6 | 578 | 22 | AAI44502 | Probe #13188 used | C 493 | 16 | 2.6 | 1001 | 21 | AAH51555 | Human PMO related |
| C 421 | 16 | 2.6 | 578 | 24 | ABO60695 | Human colon cancer | C 494 | 16 | 2.6 | 1023 | 24 | ABK63419 | DNA encoding soybe |
| C 422 | 16 | 2.6 | 583 | 23 | ABV53735 | Human prostate exp | C 495 | 16 | 2.6 | 1026 | 21 | AAAF21781 | Human breast and o |
| C 423 | 16 | 2.6 | 583 | 22 | AAK11783 | Human brain expres | C 496 | 16 | 2.6 | 1041 | 22 | AAK40812 | Human cDNA encoding nove |
| C 424 | 16 | 2.6 | 583 | 22 | AAI43384 | Probe #12070 used | C 497 | 16 | 2.6 | 1073 | 21 | AAK93425 | Human secreted pro |
| C 425 | 16 | 2.6 | 584 | 22 | AAH10769 | Human CDNA clone (| C 498 | 16 | 2.6 | 1118 | 20 | AAZ16916 | Human gene express |
| C 426 | 16 | 2.6 | 586 | 24 | ABO53376 | Oligonucleotide fo | C 499 | 16 | 2.6 | 1236 | 23 | AAAD1382 | Amplicon 6, 668int |
| C 427 | 16 | 2.6 | 586 | 24 | ABO53377 | Oligonucleotide fo | C 500 | 16 | 2.6 | 1243 | 23 | ABK20009 | Drosophila melanog |
| C 428 | 16 | 2.6 | 586 | 24 | ABK62587 | Human foetal liver | C 501 | 16 | 2.6 | 1255 | 25 | ABK59926 | Human musculoskele |
| C 429 | 16 | 2.6 | 588 | 22 | ABK29912 | Probe #8378 for ge | C 502 | 16 | 2.6 | 1269 | 20 | AAK20328 | cDNA encoding nove |
| C 430 | 16 | 2.6 | 598 | 22 | AAK10945 | Human bone marrow | C 503 | 16 | 2.6 | 1272 | 24 | AAK16976 | Borrelia burgdorfe |
| C 431 | 16 | 2.6 | 598 | 22 | AAK36797 | Human genome-deriv | C 504 | 16 | 2.6 | 1272 | 24 | AAK16977 | Human angiogenic a |
| C 432 | 16 | 2.6 | 598 | 22 | AAI17651 | Probe #7584 for ge | C 505 | 16 | 2.6 | 1278 | 24 | AAK16966 | Human angiogenic a |
| C 433 | 16 | 2.6 | 598 | 22 | AAI42578 | Probe #11264 used | C 506 | 16 | 2.6 | 1287 | 24 | AAK16966 | Human angiogenic a |
| C 434 | 16 | 2.6 | 598 | 23 | ABK36462 | Human liver single | C 507 | 16 | 2.6 | 1318 | 22 | AAK1532 | Human polynucleoti |
| C 435 | 16 | 2.6 | 598 | 24 | ABK10802 | Human genome-deriv | C 508 | 16 | 2.6 | 1319 | 24 | ABK4662 | Human cDNA differe |
| C 436 | 16 | 2.6 | 603 | 22 | AAH68909 | Human cervical can | C 509 | 16 | 2.6 | 1323 | 22 | AAK08464 | Streptococcus poly |
| C 437 | 16 | 2.6 | 604 | 22 | AAH83029 | DNA encoding G pro | C 510 | 16 | 2.6 | 1323 | 22 | AAK08464 | Human secreted pro |
| C 438 | 16 | 2.6 | 609 | 22 | AAH80055 | Peppermint plant c | C 511 | 16 | 2.6 | 1335 | 22 | AAK67011 | Human immune/haema |
| C 439 | 16 | 2.6 | 613 | 23 | ABV51891 | Human prostate exp | C 512 | 16 | 2.6 | 1345 | 22 | AAK67011 | Human secreted pro |
| C 440 | 16 | 2.6 | 615 | 24 | ABK51970 | Corn cDNA clone cc | C 513 | 16 | 2.6 | 1347 | 24 | ABK67011 | Streptococcus poly |
| C 441 | 16 | 2.6 | 615 | 25 | ABK93206 | cDNA encoding corn | C 514 | 16 | 2.6 | 1356 | 24 | ABO54719 | Human ovarian anti |
| C 442 | 16 | 2.6 | 630 | 24 | ABO39398 | Oligonucleotide fo | C 515 | 16 | 2.6 | 1367 | 21 | AAK35012 | Arabidopsis thalia |
| C 443 | 16 | 2.6 | 630 | 24 | ABO39399 | Oligonucleotide fo | C 516 | 16 | 2.6 | 1370 | 22 | AAI69877 | Human protein 17 c |
| C 444 | 16 | 2.6 | 633 | 24 | ABK66363 | Streptococcus poly | C 517 | 16 | 2.6 | 1382 | 23 | ABK42366 | Genomic sequence # |
| C 445 | 16 | 2.6 | 633 | 24 | ABN70300 | Streptococcus poly | C 518 | 16 | 2.6 | 1400 | 22 | AAK22791 | Human cDNA encodin |
| C 446 | 16 | 2.6 | 640 | 22 | AAI98588 | Human excretory re | C 519 | 16 | 2.6 | 1416 | 24 | AAK16973 | Human recombinant |

| | | | | | | |
|-------|----|-----|------|----|----------|---------------------|
| C 520 | 16 | 2.6 | 1428 | 24 | AA516971 | Human recombinant |
| C 521 | 16 | 2.6 | 1434 | 21 | AA59740 | Human secreted pro |
| C 522 | 16 | 2.6 | 1434 | 25 | AB273345 | Secreted protein-e |
| C 523 | 16 | 2.6 | 1434 | 25 | AB265953 | Human secreted pro |
| C 524 | 16 | 2.6 | 1460 | 23 | AB16339 | Drosophila melanog |
| C 525 | 16 | 2.6 | 1471 | 22 | AA522543 | Human cDNA encodin |
| C 526 | 16 | 2.6 | 1480 | 22 | AAK94095 | Human full-length |
| C 527 | 16 | 2.6 | 1492 | 22 | AAH54313 | S. epidermidis gen |
| C 528 | 16 | 2.6 | 1498 | 23 | AB155389 | Human serine oxida |
| C 529 | 16 | 2.6 | 1518 | 24 | AB231728 | Candida albicans e |
| C 530 | 16 | 2.6 | 1545 | 24 | AB067136 | Human angiogenesis |
| C 531 | 16 | 2.6 | 1552 | 21 | AAZ50890 | Human receptor-ass |
| C 532 | 16 | 2.6 | 1566 | 25 | ABX63141 | Human cDNA #141 di |
| C 533 | 16 | 2.6 | 1575 | 23 | AA553208 | Enterococcus faeca |
| C 534 | 16 | 2.6 | 1584 | 24 | ABK74549 | Bacillus licheniflo |
| C 535 | 16 | 2.6 | 1590 | 23 | AB120175 | Drosophila melanog |
| C 536 | 16 | 2.6 | 1591 | 21 | AAZ95204 | Human UGT2B7 exon |
| C 537 | 16 | 2.6 | 1605 | 24 | ABQ69120 | Listeria monocytog |
| C 538 | 16 | 2.6 | 1641 | 20 | AAK13519 | Enterococcus faeca |
| C 539 | 16 | 2.6 | 1641 | 24 | AB599314 | Enterococcus faeca |
| C 540 | 16 | 2.6 | 1659 | 22 | AAH72850 | Human cervical can |
| C 541 | 16 | 2.6 | 1660 | 23 | AA584983 | DNA encoding novel |
| C 542 | 16 | 2.6 | 1661 | 12 | AAQ12398 | Human hepatocyte g |
| C 543 | 16 | 2.6 | 1661 | 13 | AAQ22144 | Human HGF gene par |
| C 544 | 16 | 2.6 | 1661 | 12 | AAH44784 | Hepatocyte growth |
| C 545 | 16 | 2.6 | 1677 | 25 | ABX63140 | Human cDNA #140 di |
| C 546 | 16 | 2.6 | 1679 | 22 | AA512436 | DNA encoding 1-ami |
| C 547 | 16 | 2.6 | 1679 | 22 | AA512440 | HGF-WSP hybrid pro |
| C 548 | 16 | 2.6 | 1692 | 20 | AAK87663 | Human recombinant |
| C 549 | 16 | 2.6 | 1695 | 24 | AA516965 | Human T cell recep |
| C 550 | 16 | 2.6 | 1708 | 22 | ABA09166 | Borrelia burgdorfe |
| C 551 | 16 | 2.6 | 1717 | 20 | AAK20311 | Hepatocyte growth |
| C 552 | 16 | 2.6 | 1725 | 20 | AAK87662 | Human secreted pro |
| C 553 | 16 | 2.6 | 1750 | 22 | AA501461 | DNA encoding novel |
| C 554 | 16 | 2.6 | 1772 | 23 | AA586242 | Human nervous syst |
| C 555 | 16 | 2.6 | 1779 | 22 | ABA19142 | Genomic sequence # |
| C 556 | 16 | 2.6 | 1799 | 22 | AA528340 | Human nervous syst |
| C 557 | 16 | 2.6 | 1827 | 22 | ABA19141 | Genomic sequence # |
| C 558 | 16 | 2.6 | 1839 | 22 | AA528339 | Human nervous syst |
| C 559 | 16 | 2.6 | 1780 | 22 | AA580222 | DNA encoding novel |
| C 560 | 16 | 2.6 | 1798 | 22 | AAH15479 | Human cDNA sequenc |
| C 561 | 16 | 2.6 | 1805 | 22 | AAH17391 | Human cDNA sequenc |
| C 562 | 16 | 2.6 | 1827 | 24 | AB551815 | Novel human thromb |
| C 563 | 16 | 2.6 | 1839 | 22 | AA102708 | Human reproductive |
| C 564 | 16 | 2.6 | 1861 | 22 | AAH17437 | Human cDNA sequenc |
| C 565 | 16 | 2.6 | 1867 | 23 | ABV21406 | Human prostate exp |
| C 566 | 16 | 2.6 | 1867 | 23 | ABV27224 | Human prostate exp |
| C 567 | 16 | 2.6 | 1883 | 23 | AB155593 | Drosophila melanog |
| C 568 | 16 | 2.6 | 1884 | 24 | AB214431 | Arabidopsis thalia |
| C 569 | 16 | 2.6 | 1901 | 22 | AAH15963 | Human cDNA sequenc |
| C 570 | 16 | 2.6 | 1929 | 24 | AB213304 | Arabidopsis thalia |
| C 571 | 16 | 2.6 | 1938 | 23 | AB554948 | cDNA encoding huma |
| C 572 | 16 | 2.6 | 1956 | 21 | AAAZ7325 | Impatiens balsamita |
| C 573 | 16 | 2.6 | 1980 | 20 | AAK58808 | Human leukaemia-as |
| C 574 | 16 | 2.6 | 1983 | 22 | AAH18363 | Human cDNA sequenc |
| C 575 | 16 | 2.6 | 1984 | 22 | AAH16379 | Human cDNA sequenc |
| C 576 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 577 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 578 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 579 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 580 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 581 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 582 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 583 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 584 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 585 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 586 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 587 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 588 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 589 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 590 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 591 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |
| C 592 | 16 | 2.6 | 2000 | 24 | AB216512 | Arabidopsis thalia |

| | | | | | | |
|-------|----|-----|------|----|-----------|-----------------------|
| C 666 | 16 | 2.6 | 2758 | 24 | ABN99426 | Human secreted pro |
| C 667 | 16 | 2.6 | 2775 | 23 | ABL20701 | Drosophila melanog |
| C 668 | 16 | 2.6 | 2791 | 24 | ABO70805 | Listeria monocytog |
| C 669 | 16 | 2.6 | 2795 | 23 | ABLI6644 | Drosophila melanog |
| C 670 | 16 | 2.6 | 2816 | 21 | AAFC0049 | Human secreted pro |
| C 671 | 16 | 2.6 | 2818 | 20 | AAx87710 | Human Burkitt's ly |
| C 672 | 16 | 2.6 | 2824 | 25 | ABZ42633 | Human CXC chemokin |
| C 673 | 16 | 2.6 | 2969 | 22 | AAI66551 | Human iron-sulphur |
| C 674 | 16 | 2.6 | 3011 | 22 | AAH72579 | Human cervical can |
| C 675 | 16 | 2.6 | 3011 | 24 | AA594899 | Human DNA sequence |
| C 676 | 16 | 2.6 | 3108 | 24 | ABO84185 | Human P structural |
| C 677 | 16 | 2.6 | 3178 | 20 | AAx99865 | Human secreted pro |
| C 678 | 16 | 2.6 | 3178 | 22 | AA599289 | Human CDNA encodin |
| C 679 | 16 | 2.6 | 3178 | 24 | ABA90958 | Human polynucleoti |
| C 680 | 16 | 2.6 | 3202 | 24 | ABK69861 | Human secreted pro |
| C 681 | 16 | 2.6 | 3220 | 23 | ABLI30318 | Drosophila melanog |
| C 682 | 16 | 2.6 | 3220 | 23 | ABLI30318 | Drosophila melanog |
| C 683 | 16 | 2.6 | 3301 | 24 | ABV78035 | Human polynucleoti |
| C 684 | 16 | 2.6 | 3309 | 24 | ABV78035 | Hypoxia-regulated |
| C 685 | 16 | 2.6 | 3316 | 21 | ACC68344 | DNA sequence assoc |
| C 686 | 16 | 2.6 | 3327 | 25 | ACC68344 | Human dihydropyrim |
| C 687 | 16 | 2.6 | 3351 | 22 | AAI36251 | Human musculoskele |
| C 688 | 16 | 2.6 | 3351 | 25 | ABX59229 | CDNA encoding nove |
| C 689 | 16 | 2.6 | 3378 | 23 | ABLI20008 | Drosophila melanog |
| C 690 | 16 | 2.6 | 3381 | 22 | AAI02709 | Human reproductive |
| C 691 | 16 | 2.6 | 3421 | 18 | AAV74648 | Staphylococcus aur |
| C 692 | 16 | 2.6 | 3432 | 25 | ABZ10068 | Haematopoietic cel |
| C 693 | 16 | 2.6 | 3432 | 25 | ABZ10214 | Haematopoietic cel |
| C 694 | 16 | 2.6 | 3473 | 22 | AAH16188 | Human CDNA sequenc |
| C 695 | 16 | 2.6 | 3495 | 20 | AAx33814 | Coding sequence fo |
| C 696 | 16 | 2.6 | 3496 | 24 | ABLI61086 | RNA uncoupling enzy |
| C 697 | 16 | 2.6 | 3517 | 22 | ABK80466 | Human immune/haema |
| C 698 | 16 | 2.6 | 3543 | 23 | ABLI24436 | Drosophila melanog |
| C 699 | 16 | 2.6 | 3590 | 23 | ABLI20174 | Drosophila melanog |
| C 700 | 16 | 2.6 | 3599 | 24 | AA594825 | Human DNA sequence |
| C 701 | 16 | 2.6 | 3620 | 22 | ABN09117 | Human Burkitt's lymph |
| C 702 | 16 | 2.6 | 3649 | 22 | ABD05122 | Human secreted pro |
| C 703 | 16 | 2.6 | 3714 | 24 | ABK35664 | Gene LBR different |
| C 704 | 16 | 2.6 | 3714 | 24 | ABK35664 | DNA encoding Dros |
| C 705 | 16 | 2.6 | 3731 | 22 | AA557140 | Drosophila melanog |
| C 706 | 16 | 2.6 | 3731 | 23 | ABLI14232 | DNA encoding novel |
| C 707 | 16 | 2.6 | 3759 | 23 | AA576295 | DNA encoding novel |
| C 708 | 16 | 2.6 | 3795 | 20 | AA225348 | Mouse DRM nucleoti |
| C 709 | 16 | 2.6 | 3825 | 22 | AAH54430 | S. epidermidis gen |
| C 710 | 16 | 2.6 | 3825 | 23 | ABLI19976 | Drosophila melanog |
| C 711 | 16 | 2.6 | 3842 | 23 | ABLI02700 | Drosophila melanog |
| C 712 | 16 | 2.6 | 3855 | 12 | AAQ13287 | P. dentrificans ge |
| C 713 | 16 | 2.6 | 3942 | 20 | AAx99550 | Nucleic acid sequ |
| C 714 | 16 | 2.6 | 3988 | 21 | AAFC68342 | Rat insulin recept |
| C 715 | 16 | 2.6 | 3996 | 23 | ABLI03980 | Drosophila melanog |
| C 716 | 16 | 2.6 | 4000 | 22 | AAK86363 | Human immune/haema |
| C 717 | 16 | 2.6 | 4001 | 22 | AAK86364 | Human immune/haema |
| C 718 | 16 | 2.6 | 4009 | 23 | ABV24929 | Human immune/haema |
| C 719 | 16 | 2.6 | 4009 | 23 | ABV25228 | Human prostate exp |
| C 720 | 16 | 2.6 | 4017 | 23 | AA583768 | DNA encoding novel |
| C 721 | 16 | 2.6 | 4020 | 22 | AAI06054 | Human testicular a |
| C 722 | 16 | 2.6 | 4077 | 22 | AAH18537 | Human CDNA sequenc |
| C 723 | 16 | 2.6 | 4077 | 22 | AAH18537 | Human immune/haema |
| C 724 | 16 | 2.6 | 4214 | 22 | AAK72317 | DNA encoding novel |
| C 725 | 16 | 2.6 | 4358 | 22 | AAK68397 | Human immune/haema |
| C 726 | 16 | 2.6 | 4359 | 23 | AA578986 | Drosophila melanog |
| C 727 | 16 | 2.6 | 4380 | 23 | ABLI28156 | Drosophila melanog |
| C 728 | 16 | 2.6 | 4504 | 23 | ABLI05226 | Drosophila melanog |
| C 729 | 16 | 2.6 | 4528 | 22 | AAH26937 | Trichoderma reesei |
| C 730 | 16 | 2.6 | 4528 | 24 | AAH26937 | Trichoderma reesei |
| C 731 | 16 | 2.6 | 4602 | 23 | ABLI1382 | Drosophila melanog |
| C 732 | 16 | 2.6 | 4609 | 22 | AA526889 | Beet necrotic yell |
| C 733 | 16 | 2.6 | 4661 | 24 | ABQ67021 | Human angiogenesis |
| C 734 | 16 | 2.6 | 4761 | 23 | ABLI14956 | Drosophila melanog |
| C 735 | 16 | 2.6 | 4845 | 23 | ABLI20700 | Drosophila melanog |
| C 736 | 16 | 2.6 | 4896 | 24 | AAH43974 | Bacillus thuringie |
| C 737 | 16 | 2.6 | 4976 | 23 | ABLI07312 | Drosophila melanog |
| C 738 | 16 | 2.6 | 5040 | 20 | AAx20272 | Borrelia burgdorfe |
| C 739 | 16 | 2.6 | 5046 | 22 | AAH48716 | T. thermophila tri |
| C 740 | 16 | 2.6 | 5075 | 23 | ABLI30321 | Drosophila melanog |
| C 741 | 16 | 2.6 | 5099 | 24 | AAH29643 | Arabidopsis thalia |
| C 742 | 16 | 2.6 | 5099 | 24 | ABAI91396 | Arabidopsis thalis |
| C 743 | 16 | 2.6 | 5160 | 21 | AAAF21033 | Human low adenosin |
| C 744 | 16 | 2.6 | 5160 | 21 | AAAF21033 | Human adenosine re |
| C 745 | 16 | 2.6 | 5160 | 24 | ABK84262 | Human CDNA differe |
| C 746 | 16 | 2.6 | 5183 | 22 | AA545506 | Chemically pretrea |
| C 747 | 16 | 2.6 | 5183 | 24 | ABLI33349 | Human immune syste |
| C 748 | 16 | 2.6 | 5183 | 24 | ABK28438 | DNA transcription |
| C 749 | 16 | 2.6 | 5185 | 24 | ABLI30334 | Human immune syste |
| C 750 | 16 | 2.6 | 5221 | 24 | ABLI3914 | Human immune syste |
| C 751 | 16 | 2.6 | 5236 | 24 | ABLI32350 | Human immune syste |
| C 752 | 16 | 2.6 | 5299 | 22 | AA557120 | DNA encoding Dros |
| C 753 | 16 | 2.6 | 5299 | 23 | ABLI1080 | Drosophila melanog |
| C 754 | 16 | 2.6 | 5303 | 24 | ABLI3870 | Human immune syste |
| C 755 | 16 | 2.6 | 5332 | 23 | ABLI12460 | Drosophila melanog |
| C 756 | 16 | 2.6 | 5356 | 24 | ABLI70441 | Chemically treated |
| C 757 | 16 | 2.6 | 5460 | 24 | ABLI33904 | Human immune syste |
| C 758 | 16 | 2.6 | 5506 | 22 | AAK69689 | Human immune/haema |
| C 759 | 16 | 2.6 | 5728 | 24 | ABK31472 | Signal transductio |
| C 760 | 16 | 2.6 | 5769 | 24 | ABQ70951 | Listeria monocytog |
| C 761 | 16 | 2.6 | 5771 | 24 | ABLI33951 | Human immune syste |
| C 762 | 16 | 2.6 | 5798 | 24 | ABQ67012 | Human angiogenesis |
| C 763 | 16 | 2.6 | 5798 | 24 | ABLI32169 | Human immune syste |
| C 764 | 16 | 2.6 | 5844 | 24 | ABLI49390 | Human polynucleoti |
| C 765 | 16 | 2.6 | 5855 | 20 | AAI13042 | Enterococcus faeca |
| C 766 | 16 | 2.6 | 5855 | 24 | AB598837 | Enterococcus faeca |
| C 767 | 16 | 2.6 | 5898 | 24 | ABN97213 | Gene #3711 used to |
| C 768 | 16 | 2.6 | 5942 | 24 | ABLI70534 | Chemically treated |
| C 769 | 16 | 2.6 | 5942 | 24 | ABK33945 | Human DNA for stag |
| C 770 | 16 | 2.6 | 5942 | 24 | AA561135 | Human gene regulat |
| C 771 | 16 | 2.6 | 5942 | 24 | ABK31223 | Signal transductio |
| C 772 | 16 | 2.6 | 5942 | 25 | ABZ10002 | Haematopoietic cel |
| C 773 | 16 | 2.6 | 5942 | 25 | ABZ10088 | Haematopoietic cel |
| C 774 | 16 | 2.6 | 5942 | 25 | ABZ10148 | Haematopoietic cel |
| C 775 | 16 | 2.6 | 5942 | 25 | ABZ10234 | Haematopoietic cel |
| C 776 | 16 | 2.6 | 5945 | 24 | ABLI32084 | Human immune syste |
| C 777 | 16 | 2.6 | 5958 | 24 | ABLI3059 | Human immune syste |
| C 778 | 16 | 2.6 | 5962 | 24 | ABLI33468 | Human immune syste |
| C 779 | 16 | 2.6 | 5990 | 22 | AAK67673 | Human immune/haema |
| C 780 | 16 | 2.6 | 5999 | 24 | ABLI32853 | Human immune syste |
| C 781 | 16 | 2.6 | 5999 | 24 | ABK28192 | DNA transcription |
| C 782 | 16 | 2.6 | 6000 | 24 | ABK28999 | Bugula neritina PK |
| C 783 | 16 | 2.6 | 6030 | 24 | AA561347 | DNA transcription |
| C 784 | 16 | 2.6 | 6030 | 24 | ABK28311 | Human immune syste |
| C 785 | 16 | 2.6 | 6048 | 24 | ABLI4031 | Human immune syste |
| C 786 | 16 | 2.6 | 6048 | 24 | AA563353 | Chemically pretrea |
| C 787 | 16 | 2.6 | 6062 | 24 | ABLI4079 | Human immune syste |
| C 788 | 16 | 2.6 | 6076 | 24 | ABK28347 | DNA transcription |
| C 789 | 16 | 2.6 | 6092 | 22 | AA546714 | Tumour suppressor |
| C 790 | 16 | 2.6 | 6092 | 24 | AA561080 | Human gene regulat |
| C 791 | 16 | 2.6 | 6115 | 24 | ABLI33801 | Human immune syste |
| C 792 | 16 | 2.6 | 6134 | 22 | AAI169936 | CDNA encoding nove |
| C 793 | 16 | 2.6 | 6134 | 25 | ABX59924 | Human immune syste |
| C 794 | 16 | 2.6 | 6151 | 24 | ABLI3610 | DNA transcription |
| C 795 | 16 | 2.6 | 6151 | 24 | ABK28275 | Chemically treated |
| C 796 | 16 | 2.6 | 6154 | 24 | ABLI70167 | Human gene regulat |
| C 797 | 16 | 2.6 | 6154 | 24 | AA561112 | Signal transductio |
| C 798 | 16 | 2.6 | 6154 | 24 | ABK31200 | Human immune syste |
| C 799 | 16 | 2.6 | 6164 | 24 | ABLI32039 | Human immune syste |
| C 800 | 16 | 2.6 | 6171 | 24 | ABLI33011 | Human immune syste |
| C 801 | 16 | 2.6 | 6182 | 24 | ABLI34014 | Human immune syste |
| C 802 | 16 | 2.6 | 6187 | 23 | ABLI24052 | Drosophila melanog |
| C 803 | 16 | 2.6 | 6230 | 23 | ABLI02216 | CDNA sequence #501 |
| C 804 | 16 | 2.6 | 6230 | 23 | ABK36110 | Tumour suppressor |
| C 805 | 16 | 2.6 | 6274 | 24 | AA546728 | Human immune syste |
| C 806 | 16 | 2.6 | 6277 | 22 | ABK36110 | Human immune syste |
| C 807 | 16 | 2.6 | 6277 | 22 | ABLI34040 | Enterococcus faeca |
| C 808 | 16 | 2.6 | 6285 | 20 | AAI13352 | Enterococcus faeca |
| C 809 | 16 | 2.6 | 6285 | 24 | AB599147 | Drosophila melanog |
| C 810 | 16 | 2.6 | 6342 | 23 | ABLI5592 | Human immune syste |
| C 811 | 16 | 2.6 | 6396 | 24 | ABLI34247 | Human immune syste |

| | | | | | | | | | | | | | |
|-----|----|-----|------|----|-----------|---------------------|-------|----|-----|-------|----|----------|--------------------|
| 812 | 16 | 2.6 | 6418 | 24 | ABL32323 | Human immune syste | C 885 | 16 | 2.6 | 9481 | 22 | ABA20646 | Human nervous syst |
| 813 | 16 | 2.6 | 6418 | 24 | AAS61074 | Human gene regulat | C 886 | 16 | 2.6 | 9481 | 22 | AAS41696 | Genomic sequence # |
| 814 | 16 | 2.6 | 6428 | 22 | ABK78562 | Human immune/haema | C 887 | 16 | 2.6 | 9656 | 22 | AAS46524 | Tumour suppressor |
| 815 | 16 | 2.6 | 6431 | 24 | ABO67120 | Human angiogenesis | C 888 | 16 | 2.6 | 9656 | 24 | ABN80213 | Human chemically m |
| 816 | 16 | 2.6 | 6432 | 22 | AAS46558 | Tumour suppressor | C 889 | 16 | 2.6 | 9722 | 22 | ABA15166 | Human nervous syst |
| 817 | 16 | 2.6 | 6534 | 24 | ABL32471 | Human immune syste | C 890 | 16 | 2.6 | 9848 | 23 | ABL10538 | Drosophila melanog |
| 818 | 16 | 2.6 | 6544 | 22 | AAS45341 | Chemically pretrea | C 891 | 16 | 2.6 | 9876 | 24 | ABL32093 | Human immune syste |
| 819 | 16 | 2.6 | 6544 | 24 | ABL32647 | Human immune syste | C 892 | 16 | 2.6 | 9885 | 23 | ABL16338 | Drosophila melanog |
| 820 | 16 | 2.6 | 6558 | 23 | ABL12566 | Drosophila melanog | C 893 | 16 | 2.6 | 9889 | 23 | ABL07368 | Drosophila melanog |
| 821 | 16 | 2.6 | 6565 | 22 | AAS46466 | Tumour suppressor | C 894 | 16 | 2.6 | 9929 | 22 | ABA17906 | Human nervous syst |
| 822 | 16 | 2.6 | 6565 | 24 | ABK31327 | Signal transductio | C 895 | 16 | 2.6 | 10090 | 23 | ABL10760 | Drosophila melanog |
| 823 | 16 | 2.6 | 6609 | 24 | ABN80246 | Human chemically m | C 896 | 16 | 2.6 | 10100 | 23 | ABL29778 | Drosophila melanog |
| 824 | 16 | 2.6 | 6609 | 24 | ABL33882 | Human immune syste | C 897 | 16 | 2.6 | 10115 | 24 | ABK90052 | Human GSP3 genom |
| 825 | 16 | 2.6 | 6631 | 24 | ABK28339 | DNA transcription | C 898 | 16 | 2.6 | 10317 | 23 | ABL44598 | Drosophila melanog |
| 826 | 16 | 2.6 | 6699 | 24 | ABN80183 | Human chemically m | C 899 | 16 | 2.6 | 10377 | 24 | ABL34220 | Human immune syste |
| 827 | 16 | 2.6 | 6774 | 24 | ABO67155 | Human angiogenesis | C 900 | 16 | 2.6 | 10503 | 22 | AAK89097 | Human digestive sy |
| 828 | 16 | 2.6 | 6904 | 24 | ABL32212 | Human immune syste | C 901 | 16 | 2.6 | 11036 | 20 | AAK13401 | Enterococcus faeca |
| 829 | 16 | 2.6 | 6933 | 23 | ABL07454 | Drosophila melanog | C 902 | 16 | 2.6 | 11036 | 24 | ABS99196 | Enterococcus faeca |
| 830 | 16 | 2.6 | 6935 | 24 | ABL92263 | Chemically treated | C 903 | 16 | 2.6 | 11115 | 22 | AAS41967 | Genomic sequence # |
| 831 | 16 | 2.6 | 6980 | 24 | ABL32453 | Human immune syste | C 904 | 16 | 2.6 | 11115 | 22 | AAS41974 | Genomic sequence # |
| 832 | 16 | 2.6 | 7008 | 22 | AAS46531 | Tumour suppressor | C 905 | 16 | 2.6 | 11115 | 23 | ABK72139 | Human ovarian anti |
| 833 | 16 | 2.6 | 7113 | 24 | ABL32805 | Human immune syste | C 906 | 16 | 2.6 | 11115 | 24 | ABK91731 | Novel ovarian rela |
| 834 | 16 | 2.6 | 7114 | 22 | AAK70622 | Human immune/haema | C 907 | 16 | 2.6 | 11209 | 24 | ABN80137 | Human chemically m |
| 835 | 16 | 2.6 | 7115 | 22 | AAK07153 | Human reproductive | C 908 | 16 | 2.6 | 11456 | 22 | AAK69400 | Human immune/haema |
| 836 | 16 | 2.6 | 7167 | 24 | ABL32400 | Human immune syste | C 909 | 16 | 2.6 | 11907 | 24 | ABK31320 | Signal transductio |
| 837 | 16 | 2.6 | 7306 | 24 | ABO67109 | Human angiogenesis | C 910 | 16 | 2.6 | 11944 | 24 | ABL34187 | Human immune syste |
| 838 | 16 | 2.6 | 7341 | 24 | ABL33636 | Human immune syste | C 911 | 16 | 2.6 | 12000 | 24 | ABK34015 | Human DNA for stag |
| 839 | 16 | 2.6 | 7353 | 24 | ABL33073 | Human immune syste | C 912 | 16 | 2.6 | 12133 | 24 | ABN80322 | Human chemically m |
| 840 | 16 | 2.6 | 7353 | 24 | AAK28363 | Human chemically t | C 913 | 16 | 2.6 | 12237 | 24 | ABL43358 | Human immune syste |
| 841 | 16 | 2.6 | 7355 | 24 | ABN80296 | Human chemically m | C 914 | 16 | 2.6 | 12507 | 24 | ABL32298 | Human immune syste |
| 842 | 16 | 2.6 | 7403 | 22 | AAS46803 | Tumour suppressor | C 915 | 16 | 2.6 | 12693 | 22 | ABA20625 | Human nervous syst |
| 843 | 16 | 2.6 | 7403 | 22 | AAS46804 | Human immune syste | C 916 | 16 | 2.6 | 12693 | 22 | AAK79994 | Human immune/haema |
| 844 | 16 | 2.6 | 7403 | 24 | ABL34216 | Human immune syste | C 917 | 16 | 2.6 | 12808 | 23 | ABL30320 | Drosophila melanog |
| 845 | 16 | 2.6 | 7403 | 24 | ABL34217 | Human immune syste | C 918 | 16 | 2.6 | 13103 | 23 | ABL29868 | Drosophila melanog |
| 846 | 16 | 2.6 | 7500 | 24 | ABL33115 | Human immune syste | C 919 | 16 | 2.6 | 13111 | 23 | ABL13364 | Drosophila melanog |
| 847 | 16 | 2.6 | 7503 | 24 | ABO67009 | Human angiogenesis | C 920 | 16 | 2.6 | 13123 | 24 | ABL54364 | Chemically treated |
| 848 | 16 | 2.6 | 7503 | 24 | ABL33548 | Human immune syste | C 921 | 16 | 2.6 | 13123 | 24 | ABK31423 | Signal transductio |
| 849 | 16 | 2.6 | 7577 | 23 | ABL02214 | Drosophila melanog | C 922 | 16 | 2.6 | 13125 | 24 | ABL70283 | Chemically treated |
| 850 | 16 | 2.6 | 7577 | 12 | AAO15133 | Zucchini ACC synth | C 923 | 16 | 2.6 | 13125 | 24 | ABL33226 | Human immune syste |
| 851 | 16 | 2.6 | 7587 | 19 | AAV15703 | Zucchini ACC synth | C 924 | 16 | 2.6 | 13125 | 24 | ABL44556 | Human immune syste |
| 852 | 16 | 2.6 | 7587 | 22 | AAK04543 | Zucchini CP-ACC 1B | C 925 | 16 | 2.6 | 13361 | 23 | ABL17960 | Drosophila melanog |
| 853 | 16 | 2.6 | 7587 | 22 | AAF23620 | Zucchini ACC synth | C 926 | 16 | 2.6 | 13395 | 22 | AAK74325 | Human immune/haema |
| 854 | 16 | 2.6 | 7676 | 24 | ABL70409 | Chemically treated | C 927 | 16 | 2.6 | 13444 | 23 | ABL15546 | Drosophila melanog |
| 855 | 16 | 2.6 | 7676 | 24 | ABL34598 | Human metastasis a | C 928 | 16 | 2.6 | 13491 | 23 | ABL25572 | Drosophila melanog |
| 856 | 16 | 2.6 | 7793 | 25 | ABZ73859 | Secreted protein g | C 929 | 16 | 2.6 | 13548 | 21 | AAF21037 | Human low adenosin |
| 857 | 16 | 2.6 | 7793 | 25 | ABZ67436 | Human secreted pro | C 930 | 16 | 2.6 | 13548 | 21 | AAA34915 | Human adenosine re |
| 858 | 16 | 2.6 | 7829 | 24 | ABL70266 | Chemically treated | C 931 | 16 | 2.6 | 13784 | 24 | ABK40061 | Human chemically p |
| 859 | 16 | 2.6 | 7829 | 24 | ABL33105 | Human immune syste | C 932 | 16 | 2.6 | 13792 | 24 | ABL33570 | Human immune syste |
| 860 | 16 | 2.6 | 7829 | 24 | AAS61191 | Human gene regulat | C 933 | 16 | 2.6 | 14316 | 24 | ABL70606 | Chemically treated |
| 861 | 16 | 2.6 | 7829 | 24 | ABK31287 | Signal transductio | C 934 | 16 | 2.6 | 14316 | 24 | AAS61445 | Human gene regulat |
| 862 | 16 | 2.6 | 7843 | 23 | ABL28755 | Drosophila melanog | C 935 | 16 | 2.6 | 14316 | 24 | ABK31519 | Signal transductio |
| 863 | 16 | 2.6 | 7857 | 24 | ABO67075 | Human angiogenesis | C 936 | 16 | 2.6 | 14362 | 24 | ABO67048 | Human angiogenesis |
| 864 | 16 | 2.6 | 7924 | 24 | ABK40065 | Human chemically p | C 937 | 16 | 2.6 | 14494 | 23 | ABL17946 | Drosophila melanog |
| 865 | 16 | 2.6 | 7924 | 24 | ABL34138 | Human immune syste | C 938 | 16 | 2.6 | 14617 | 22 | ABA19132 | Human nervous syst |
| 866 | 16 | 2.6 | 8032 | 24 | ABL70447 | Chemically treated | C 939 | 16 | 2.6 | 14627 | 22 | ABA19130 | Human nervous syst |
| 867 | 16 | 2.6 | 8032 | 24 | AAS61408 | Human gene regulat | C 940 | 16 | 2.6 | 14708 | 22 | AAS45514 | Chemically pretrea |
| 868 | 16 | 2.6 | 8032 | 24 | ABL31478 | Signal transductio | C 941 | 16 | 2.6 | 14708 | 24 | ABL92325 | Chemically treated |
| 869 | 16 | 2.6 | 8115 | 22 | AAS41935 | Genomic sequence # | C 942 | 16 | 2.6 | 14708 | 24 | ABL34245 | Human immune syste |
| 870 | 16 | 2.6 | 8115 | 22 | AAS41947 | Genomic sequence # | C 943 | 16 | 2.6 | 14708 | 24 | ABK28450 | DNA transcription |
| 871 | 16 | 2.6 | 8115 | 22 | AAS41961 | Genomic sequence # | C 944 | 16 | 2.6 | 14855 | 22 | ABA15164 | Human nervous syst |
| 872 | 16 | 2.6 | 8115 | 22 | AAS41963 | Genomic sequence # | C 945 | 16 | 2.6 | 15247 | 24 | ABK40064 | Human chemically p |
| 873 | 16 | 2.6 | 8166 | 24 | ABL33792 | Human immune syste | C 946 | 16 | 2.6 | 15247 | 24 | ABL4083 | Human immune syste |
| 874 | 16 | 2.6 | 8237 | 22 | AAS46802 | Tumour suppressor | C 947 | 16 | 2.6 | 15396 | 23 | ABL7860 | Drosophila melanog |
| 875 | 16 | 2.6 | 8298 | 24 | ABN80190 | Human chemically m | C 948 | 16 | 2.6 | 15643 | 22 | AAS31559 | Human DNA for a no |
| 876 | 16 | 2.6 | 8486 | 24 | ABL34445 | Human immune syste | C 949 | 16 | 2.6 | 15643 | 22 | ABO66883 | Human polynucleoti |
| 877 | 16 | 2.6 | 8559 | 22 | AAI199011 | Human excretory re | C 950 | 16 | 2.6 | 15732 | 24 | AAS45388 | Chemically pretrea |
| 878 | 16 | 2.6 | 8559 | 22 | AAI63361 | Human kidney relat | C 951 | 16 | 2.6 | 15732 | 24 | ABK28233 | DNA transcription |
| 879 | 16 | 2.6 | 9000 | 24 | ABK70903 | Mouse HYPLIP1 geno | C 952 | 16 | 2.6 | 15743 | 24 | ABK28396 | DNA transcription |
| 880 | 16 | 2.6 | 9000 | 24 | ABK48677 | Genomic DNA sequen | C 953 | 16 | 2.6 | 15872 | 22 | AAS46520 | Tumour suppressor |
| 881 | 16 | 2.6 | 9084 | 24 | ABL33605 | Human immune syste | C 954 | 16 | 2.6 | 16084 | 22 | AAI36161 | Human muscle skele |
| 882 | 16 | 2.6 | 9157 | 24 | ABL33500 | Human immune syste | C 955 | 16 | 2.6 | 16084 | 25 | ABK59149 | CDNA encoding nove |
| 883 | 16 | 2.6 | 9206 | 24 | ABL33674 | Human immune syste | C 956 | 16 | 2.6 | 16896 | 23 | ABL20462 | Drosophila melanog |
| 884 | 16 | 2.6 | 9345 | 21 | AAZ93966 | Mouse utromodulin p | C 957 | 16 | 2.6 | 16914 | 24 | ABL70315 | Chemically treated |

| | | | | | | |
|--------|----|-----|-------|----|----------|---------------------|
| C 958 | 16 | 2.6 | 16914 | 24 | AA661253 | Human gene regulat |
| C 959 | 16 | 2.6 | 17656 | 24 | AB555502 | SweetImm Agamous g |
| C 960 | 16 | 2.6 | 17721 | 24 | AB133728 | Human immune syste |
| C 961 | 16 | 2.6 | 17738 | 24 | AB133539 | Human immune syste |
| C 962 | 16 | 2.6 | 17869 | 24 | ABK39921 | Human chemically p |
| C 963 | 16 | 2.6 | 17869 | 24 | ABJ32105 | Human immune syste |
| C 964 | 16 | 2.6 | 18011 | 24 | AB132035 | Human immune syste |
| C 965 | 16 | 2.6 | 18047 | 22 | AAK80292 | Human immune/haema |
| C 966 | 16 | 2.6 | 19011 | 22 | AA103125 | Human reproductive |
| C 967 | 16 | 2.6 | 19011 | 22 | AA103126 | Human reproductive |
| C 968 | 16 | 2.6 | 19011 | 22 | AAK84511 | Human immune/haema |
| C 969 | 16 | 2.6 | 19011 | 22 | AAK84512 | Human immune/haema |
| C 970 | 16 | 2.6 | 19082 | 24 | AB132626 | Human immune syste |
| C 971 | 16 | 2.6 | 19236 | 24 | ABN80226 | Human chemically m |
| C 972 | 16 | 2.6 | 19369 | 22 | AAK65309 | Human immune/haema |
| C 973 | 16 | 2.6 | 20598 | 22 | AAK24851 | Nucleotide sequenc |
| C 974 | 16 | 2.6 | 20598 | 24 | AAK24851 | Human zaiplna3 gen |
| C 975 | 16 | 2.6 | 20746 | 22 | AA107353 | Human reproductive |
| C 976 | 16 | 2.6 | 21354 | 22 | AAK46784 | Tumour suppressor |
| C 977 | 16 | 2.6 | 21354 | 22 | AAK46786 | Tumour suppressor |
| C 978 | 16 | 2.6 | 22028 | 24 | ABA93286 | Human acetyl-Coenz |
| C 979 | 16 | 2.6 | 22028 | 24 | ABA93288 | Human acetyl-Coenz |
| C 980 | 16 | 2.6 | 23203 | 23 | AB117834 | Drosophila melanog |
| C 981 | 16 | 2.6 | 24939 | 22 | AAK65622 | Human immune/haema |
| C 982 | 16 | 2.6 | 25002 | 24 | ABQ74278 | C. elegans Z92825 |
| C 983 | 16 | 2.6 | 25423 | 22 | AAK90279 | Human digestive sy |
| C 984 | 16 | 2.6 | 25423 | 22 | AA157656 | Human colorectal c |
| C 985 | 16 | 2.6 | 25423 | 24 | AB599833 | Genomic DNA #37 en |
| C 986 | 16 | 2.6 | 25424 | 22 | AAK90280 | Human digestive sy |
| C 987 | 16 | 2.6 | 25424 | 22 | AA157657 | Human colorectal c |
| C 988 | 16 | 2.6 | 25424 | 24 | AB599834 | Genomic DNA #38 en |
| C 989 | 16 | 2.6 | 25911 | 23 | AB102604 | Drosophila melanog |
| C 990 | 16 | 2.6 | 25929 | 23 | AB102602 | Drosophila melanog |
| C 991 | 16 | 2.6 | 26016 | 19 | AAV52722 | Human flavin-conta |
| C 992 | 16 | 2.6 | 26496 | 22 | AB119656 | Human nervous syst |
| C 993 | 16 | 2.6 | 27571 | 22 | AB119657 | Human nervous syst |
| C 994 | 16 | 2.6 | 27572 | 22 | AB119221 | Human nervous syst |
| C 995 | 16 | 2.6 | 28001 | 24 | AB554410 | Human hydroxymethyl |
| C 996 | 16 | 2.6 | 28001 | 25 | ABK93300 | Gene encoding huma |
| C 997 | 16 | 2.6 | 28313 | 22 | AA136829 | Human musculoskele |
| C 998 | 16 | 2.6 | 28313 | 25 | ABK59817 | CDNA encoding nove |
| C 999 | 16 | 2.6 | 28432 | 23 | AB105010 | Drosophila melanog |
| C 1000 | 16 | 2.6 | 28506 | 24 | ABK90191 | Human flavin conta |

ALIGNMENTS

RESULT 1
ID ABK97884
XX ABK97884 standard; DNA; 622 BP.

AC ABK97884;
XX

DT 10-OCT-2002 (first entry)
XX

DE DNA encoding Lawsonia intracellularis antigenic flhB protein.
XX

XX Immunogen; flhB; flhR; ntrC; glhH; motB; clyC; yfem; yfem;
XX porcine; pig; avian; bird; porcine proliferative enteropathy; PPE;
XX intestinal adenomatosis complex; porcine intestinal adenomatosis;
XX PIA; necrotic enteritis; proliferative haemorrhagic enteropathy;
XX regional ileitis; haemorrhagic bowel syndrome; vaccine; antibacterial;
XX porcine proliferative enteritis; Campylobacter spp.-induced enteritis;
XX gene; de.

XX Lawsonia intracellularis.
XX

PN WO200238594-A1.
XX

PD 16-MAY-2002.
XX

PF 09-NOV-2001; 2001WO-AU01462.
XX

XX 10-NOV-2000; 2000AU-0001381.
PR 17-NOV-2000; 2000US-249596P.
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AUPO-) AUSTRALIAN PORK LTD.
PA (PFIZ) PFIZER PROD INC.
XX Rosey EL, King KW, Good RT, Strugnelli RA;
XX WPI; 2002-557448/59.
DR P-PSDB; ABG689910.
XX

PT New immunogenic polypeptide comprising epitope of Lawsonia spp.
PT polypeptide such as flhB, flhR, ntrC, glhH, motB, polyepitope, useful
PT in vaccines for treatment of porcine proliferative enteropathy in pigs
PT and birds

PS Claim 6; Page 99-100; 155pp; English.

XX The invention describes an isolated or recombinant immunogenic
CC polypeptide (I) which comprises, mimics or cross-reacts with a B-cell or
CC T-cell epitope of a Lawsonia spp. polypeptide such as flhB, flhR, ntrC,
CC glhH, motB, clyC, yfem or yfem polypeptides. (I) is useful for
CC identifying whether or not a porcine or avian animal has suffered from a
CC past infection, or is currently infected, with Lawsonia spp. or a
CC microorganism that is immunologically cross-reactive with Lawsonia spp.
CC Antibodies are useful for diagnosing infection of a porcine or avian
CC animal by Lawsonia spp. or a microorganism that is immunologically
CC cross-reactive with Lawsonia spp.. A nucleic acid encoding a Lawsonia
CC spp. immunogen is useful as probes or primers for detecting Lawsonia spp.
CC or related microorganism in a biological sample derived from a porcine or
CC avian animal subject. (I) is preferably useful for vaccinating porcine
CC animals against intestinal diseases collectively known as intestinal
CC proliferative enteropathy (PPE), previously known as intestinal
CC adenomatosis complex, porcine intestinal adenomatosis (PIA), necrotic
CC enteritis, proliferative haemorrhagic enteropathy, regional ileitis,
CC haemorrhagic bowel syndrome, porcine proliferative enteritis and
CC Campylobacter spp.-induced enteritis. (I) is also useful in vaccines for
CC the prophylaxis and treatment of PPE in birds. This sequence encodes a
CC Lawsonia intracellularis immunogenic peptide used in the creation of a
CC porcine vaccine described in the invention.

SQ Sequence 622 BP; 189 A; 92 C; 123 G; 218 T; 0 other;

Query Match 100.0%; Score 622; DB 24; Length 622;
Best Local Similarity. 100.0%; Pred. No. 1.5e-252;
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | ATGCTGATGATCCAGTAAACAGAGAAGCAACCCGGAACGACGTGAGAGCTCGT | 60 |
| DB | 1 | ATGCTGATGATCCAGTAAACAGAGAAGCAACCCGGAACGACGTGAGAGCTCGT | 60 |
| QY | 61 | TCTGAAGGAGTGTCCCTAAATCAGAGAAGGTTACTAAGACTGACTGACAGAGG | 120 |
| DB | 61 | TCTGAAGGAGTGTCCCTAAATCAGAGAAGGTTACTAAGACTGACTGACAGAGG | 120 |
| QY | 121 | ATGCTGGGGCTTCTATTATTATTCAGGGTAAATGGAGCTATTGGAACAATTTTCTAC | 180 |
| DB | 121 | ATGCTGGGGCTTCTATTATTATTCAGGGTAAATGGAGCTATTGGAACAATTTTCTAC | 180 |
| QY | 181 | TATATTTTACGAATCATTTCCGTTGAGGTTACAGACAGTCAATGATGCTTATTT | 240 |
| DB | 181 | TATATTTTACGAATCATTTCCGTTGAGGTTACAGACAGTCAATGATGCTTATTT | 240 |
| QY | 241 | ATTATGTTGCTCAAGATAGCTAATTTATGATGCCAATATTACTTTTATGCTGTT | 300 |
| DB | 241 | ATTATGTTGCTCAAGATAGCTAATTTATGATGCCAATATTACTTTTATGCTGTT | 300 |
| QY | 301 | ACGGATGATTTTCAATTCGTTACAGTGTGGTATTTATGATGACAAAGGTTTAA | 360 |
| DB | 301 | ACGGATGATTTTCAATTCGTTACAGTGTGGTATTTATGATGACAAAGGTTTAA | 360 |

| | | | |
|----|-----|---|-----|
| Qy | 421 | ACACTGTTGCACTTTACGTAAGTTAGTTCACGAATATGTTATAGTAATGTTCCATAT | 480 |
| Db | 421 | ACACTGTTGCACTTTACGTAAGTTAGTTCACGAATATGTTATAGTAATGTTCCATAT | 480 |
| Qy | 421 | ACACTGTTGCACTTTACGTAAGTTAGTTCACGAATATGTTATAGTAATGTTCCATAT | 480 |
| Qy | 481 | ATCATATATATAAGAGAGATTTTCAAACTTTTACCATATATATATGCAAGTCCTTCAGGT | 540 |
| Db | 481 | ATCATATATATAAGAGAGATTTTCAAACTTTTACCATATATATATGCAAGTCCTTCAGGT | 540 |
| Qy | 541 | GTCGCAGATTAATATGCTTAATAACAGAAATAGTACTTGTTTATATAGCGTAATTCCTATG | 600 |
| Db | 541 | GTCGCAGATTAATATGCTTAATAACAGAAATAGTACTTGTTTATATAGCGTAATTCCTATG | 600 |
| Qy | 601 | ACAATATATGCAAGTCAGATC 622 | |
| Db | 601 | ACAATATATGCAAGTCAGATC 622 | |

| | |
|----|---|
| XX | RESULT 2 |
| XX | ABV96020/c |
| ID | ABV96020 standard; cDNA; 340 BP. |
| AC | ABV96020; |
| XX | |
| DT | 14-JAN-2003 (first entry) |
| XX | |
| DE | Human pancreatic cancer expressed cDNA SEQ ID NO 1428. |
| XX | |
| KW | Human; pancreas; cancer; gene therapy; vaccine; immunostimulant; cytostatic; tumour; gene; ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO200260317-A2. |
| PD | 08-AUG-2002. |
| XX | |
| PF | 30-JAN-2002; 2002WO-US02781. |
| PR | 30-JAN-2001; 2001US-265305P. |
| PR | 31-JAN-2001; 2001US-265682P. |
| PR | 09-FEB-2001; 2001US-267568P. |
| PR | 21-MAR-2001; 2001US-278651P. |
| PR | 28-APR-2001; 2001US-287112P. |
| PR | 16-MAY-2001; 2001US-291631P. |
| PR | 12-JUL-2001; 2001US-305484P. |
| PR | 20-AUG-2001; 2001US-313999P. |
| PR | 27-NOV-2001; 2001US-333626P. |
| XX | |
| PA | (CORI-) CORIXA CORP. |
| XX | |
| PI | Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y; |
| XX | |
| DR | WPI; 2002-627435/67. |
| XX | |
| PT | New isolated polynucleotide and pancreatic tumor polypeptides, useful |
| PT | for diagnosing, preventing and/or treating cancer, particularly |
| PT | pancreatic cancer - |
| XX | |
| PS | Claim 1; SEQ ID NO 1428; 300bp + Sequence Listing; English. |
| XX | |
| CC | The invention relates to an isolated polynucleotide (1) comprising: (a) |
| CC | any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); |
| CC | (b) complements of (a); (c) sequences consisting of at least 20 |
| CC | contiguous residues of (a); (d) sequences that hybridize to (a), under |
| CC | moderately stringent conditions; (e) sequences having at least 75% or 90% |
| CC | identity to (a); or (f) degenerate variants of (a). Polypeptides |
| CC | (ABP66596-ABP66637) encoded by (1) and oligonucleotide can be used to |
| CC | detect cancer in a patient and compositions comprising polypeptides and |
| CC | polynucleotides, antibodies, fusion proteins, T cell populations and |

CC antigen presenting cells expressing the polypeptide are useful in
CC treating pancreatic cancer and stimulating an immune response. The
CC polynucleotides can be used as probes or primers for nucleic acid
CC hybridisation, in the design and preparation of ribozyme molecules for
CC inhibiting expression of the tumour polypeptides and proteins in the
CC tumour cells, in vaccines and for gene therapy.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 340 BP; 100 A; 81 C; 64 G; 94 T; 1 other;

```

Query Match      3.1%; Score 19; DB 24; Length 340;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 AGCATTTTATTATATGCCA 279
      |||||||
Db      . 307 AGCATTTTATTATATGCCA 289

```

| | |
|----|---|
| XX | RESULT 3 |
| XX | ABAS68347/c |
| ID | ABA58347 standard; DNA; 390 BP. |
| XX | |
| AC | ABA58347; |
| DT | 01-FEB-2002 (first entry) |
| XX | |
| DE | Human foetal liver single exon nucleic acid probe #6652. |
| XX | |
| KW | Human; foetal liver; gene expression; single exon nucleic acid probe; ss. |
| XX | |
| OS | Homo sapiens. |
| PN | WO200157277-A2. |
| XX | |
| PD | 09-AUG-2001. |
| XX | |
| PF | 30-JAN-2001; 2001MO-US006659. |
| XX | |
| PR | 04-FEB-2000; 2000US-0180312. |
| PR | 26-MAY-2000; 2000US-0207456. |
| PR | 30-JUN-2000; 2000US-0608408. |
| PR | 03-AUG-2000; 2000US-0632366. |
| PR | 21-SEP-2000; 2000US-0234687. |
| PR | 27-SEP-2000; 2000US-0236359. |
| PR | 04-OCT-2000; 2000GB-0024263. |
| XX | |
| PA | (MOL-E-) MOLECULAR DYNAMICS INC. |
| F1 | Penn SG, Hanzel DK, Chen W, Rank DR; |
| XX | |
| DR | WPI; 2001-483447/52. |
| XX | |
| PT | Human genome-derived single exon nucleic acid probes useful for |
| FT | analyzing gene expression in human fetal liver - |
| XX | |
| PS | Claim 1; SEQ ID NO 6652; 639pp + sequence listing; English. |
| XX | |
| CC | The invention relates to a single exon nucleic acid probe for |
| CC | measuring human gene expression in a sample derived from human foetal |
| CC | liver. The single exon nucleic acid probes may be used for predicting, |
| CC | measuring and displaying gene expression in samples derived from human |
| CC | fetal liver. The present sequence is a single exon nucleic acid |
| CC | probe of the invention. |
| CC | Note: The sequence data for this patent did not form part of the |
| CC | printed specification, but was obtained in electronic format directly |
| CC | from WIPO at ftp.wipo.int/pub/published_pct_sequences. |
| XX | |
| SQ | Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other; |

Query Match 3.1%; Score 19; DB 22; Length 390;

Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 ATATGCTTATTATTAT 246
Db 79 ATATGCTTATTATTAT 61

RESULT 4
ABA27469/c

ID ABA27469 standard; DNA; 390 BP.

AC ABA27469;

DT 23-JAN-2002 (first entry)

DE Probe #5935 for gene expression analysis in human heart cell sample.

KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488899/53.

CC Single exon nucleic acid probes for analyzing gene expression in human

CC hearts -

CC Claim 1; SEQ ID No 5935; 530pp; English.

CC The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart. The

CC present sequence is one such probe. The probes may be used for

CC predicting, measuring and displaying gene expression in samples derived

CC from the human heart via microarrays. By measuring gene expression, the

CC probes are useful for predicting, diagnosing, grading, staging,

CC monitoring and prognosing diseases of the human heart and vascular system

CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and

CC congenital heart disease.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

RESULT 5

AAK06446/c

ID AAK06446 standard; DNA; 390 BP.

AC AAK06446;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe SEQ ID NO: 6437.

KW Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer; ss.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00667.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483446/52.

CC Single exon nucleic acid probes for analyzing gene expression in human

CC brains -

CC Example 4; SEQ ID NO: 6437; 650pp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

CC epilepsy and cancers. The present sequence is one of the probes of the

CC invention.

CC Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;

CC Query Match 3.1%; Score 19; DB 22; Length 390;

CC Best Local Similarity 100.0%; Pred. No. 37;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 ATATGCTTATTATTAT 246
Db 79 ATATGCTTATTATTAT 61

RESULT 6

AAK32124/c

ID AAK32124 standard; DNA; 390 BP.

AC AAK32124;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed single exon probe SEQ ID NO: 6681.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukemia; lymphoma; myeloma; ss.

```
OS Homo sapiens.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PN WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00668.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 6681; 658bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukemia and myeloma. The present sequence is one of
XX the probes of the invention.
XX
XX SQ Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;

Query Match          3.1%; Score 19; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      228 ATATGCTTTATTATTAT 246
Db      79 ATATGCTTTATTATTAT 61

RESULT 7
AA115959/c
ID AA115959 standard; DNA; 390 BP.
XX
XX AA115959;
XX
XX 12-OCT-2001 (first entry)
XX
XX Probe #5892 for gene expression analysis in human cervical cell sample.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
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XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PN Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
XX Claim 25; SEQ ID No 5892; 487bp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
XX (SENPs). The present sequence is one such probe. The SENPs are derived
XX from human Hela cells. The SENPs can be used to produce a single exon
XX microarray, which can be used for measuring human gene expression in a
XX sample derived from human cervical epithelial cells. By measuring gene
XX expression, the probes are therefore useful in grading and/or staging
XX of diseases of the cervix, notably cervical cancer.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;

Query Match          3.1%; Score 19; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      228 ATATGCTTTATTATTAT 246
Db      79 ATATGCTTTATTATTAT 61

RESULT 8
AA137975/c
ID AA137975 standard; DNA; 390 BP.
XX
XX AA137975;
XX
XX 17-OCT-2001 (first entry)
XX
XX Probe #6661 used to measure gene expression in human placenta sample.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00663.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
XX Claim 25; SEQ ID No 6661; 654bp; English.
```

XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;
XX
Query Match 3.1%; Score 19; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 228 ATATGCTTATTATTAT 246
DB 79 ATATGCTTATTATTAT 61
XX
RESULT 9
ID ABS31820/c
XX ABS31820 standard; DNA; 390 BP.
AC
XX ABS31820;
DT 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID No 6810.
XX
XX Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
XX Homo sapiens.
OS
XX WO200157273-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US00664.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488698/53.
DR
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analysing gene expression in human adult liver -
XX
XX Claim 1; SEQ ID No 6810; 658bp; English.
PS
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (1) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult
CC liver. (1) may be used for predicting, measuring and displaying gene
CC expression in samples derived from human adult liver. The genes
CC identified may be involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
CC is associated with coronary heart disease. ABS25011-ABS51005 represent
CC human liver single exon nucleic acid probes of the invention.
CC Note: The sequence information for this patent does not appear in the
CC printed specification but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;
XX
Query Match 3.1%; Score 19; DB 23; Length 390;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 228 ATATGCTTATTATTAT 246
DB 79 ATATGCTTATTATTAT 61
XX
RESULT 10
ID ABS06891/c
XX ABS06891 standard; DNA; 390 BP.
AC
XX ABS06891;
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe from lung SEQ ID No 6882.
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenen syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
XX Homo sapiens.
OS
XX WO200186003-A2.
PN
XX 15-NOV-2001.
PD
XX 30-JAN-2001; 2001WO-US00665.
PF
XX
XX 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2002-114183/15.
DR
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
XX Claim 1; SEQ ID No 6882; 634bp; English.
PS
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridization to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 1201 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemorrhoidosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karsagen syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a single exon
CC probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WJPO at
CC ftp.wjpo.int/pub/published_pct_sequences.

XX Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;

CC Query Match 3.1%; Score 19; DB 24; Length 390;
CC Best Local Similarity 100.0%; Pred. No. 37;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 ATATGCTTATTATTAT 246
Db 79 ATATGCTTATTATTAT 61

Db 79 ATATGCTTATTATTAT 61

RESULT 11

ABN67186 standard; DNA; 693 BP.

XX ABN67186;

DT 01-JUN-2002 (first entry)

DE Streptococcus polymnucleotide SEQ ID NO 2285.

XX Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;

KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;

XX antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.

OS Streptococcus pyogenes.

XX WO200234771-A2.

PD 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB04789.

PR 27-OCT-2000; 2000GB-0026333.

PR 24-NOV-2000; 2000GB-0028727.

PR 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
XX Tettelin H;
XX WPI, 2002-352536/38.
XX P-PSDB; ABP26555.

PT New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -

XX Claim 7; Page 3379; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.

XX Sequence 693 BP; 193 A; 126 C; 171 G; 203 T; 0 other;

CC Query Match 3.1%; Score 19; DB 24; Length 693;
CC Best Local Similarity 100.0%; Pred. No. 37;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 TGATGCCAATATTACTTT 290
Db 603 TGATGCCAATATTACTTT 621

Db 603 TGATGCCAATATTACTTT 621

RESULT 12.

ACA04580 standard; cDNA; 948 BP.

XX ACA04580;

DT 28-MAY-2003 (first entry)

DE cDNA encoding human membrane associated protein fragment #28.

XX Human; sex; gene; microarray; membrane-associated protein; neuropathology;

KW immunopathology; pancreatic disease; cancer; diabetes; hyperlipidaemia;

KW pancreatic cholera; Alzheimer's disease; Huntington's disease; sarcoma;

KW fibrocystic disease; leukaemia; adenocarcinoma; AIDS; allergy; anaemia;

XX asthma; gout; dementia.

OS Homo sapiens.

XX US6492505-B1.

XX 10-DEC-2002.

XX 31-JAN-2000; 2000US-0495050.

XX 01-FEB-1999; 99US-118318P.

XX (INCY-) INCYTE GENOMICS INC.

XX Reddy R, Guegler KJ, Au-Young J;

XX WPI; 2003-327324/31.

XX Combination for research/diagnostic applications and for monitoring
XX treatment of e.g., cancer, comprises polynucleotides comprising a
XX fragment of gene encoding membrane-associated proteins, receptors or
XX ion channels -
XX Claim 1; Column 51-52; 147pp; English.

XX The invention relates to a combination comprising several polynucleotide
 CC sequences comprising a fragment of gene encoding membrane-associated
 CC proteins, receptors or ion channels. The combination is useful as a
 CC probe, for research and diagnostic applications, for monitoring the
 CC expression of several expressed polynucleotides, in the diagnosis and
 CC monitoring of treatment of pancreatic disease, cancer, immunopathology or
 CC neuropathology, for investigating an individual's predisposition to the
 CC above disease, in genetic or gene expression analysis of polynucleotide
 CC sequences, to investigate cellular responses to infection or drug
 CC treatment, as hybridizable array elements in a microarray, to purify a
 CC subpopulation of mRNAs, cDNAs or genomic fragments in a sample, in
 CC diagnostics, prognostics and treatment regimens, in drug discovery and
 CC development, in toxicological and carcinogenicity studies, and in
 CC forensic or pharmacogenomics, to monitor the progression of disease, to
 CC monitor the efficacy of treatment, to diagnose the conditions of the
 CC pancreas e.g. diabetes, pancreatic cholera, hyperlipidemia or
 CC fibrocystic disease, to diagnose a cancer e.g. leukemia, adenocarcinoma
 CC or sarcoma, to diagnose immunopathologies e.g. AIDS, allergies, anaemia,
 CC asthma or gout, to diagnose neuropathologies e.g. Alzheimer's disease,
 CC dementia or Huntington's disease, to rapidly screen large numbers of
 CC candidate drug molecules and as query sequences against GenBank,
 CC SwissProt, BLOCKS and PRINTS databases. The combination is employed to
 CC fine tune the treatment regimen and thus the expression patterns
 CC associated with undesirable side effects are avoided. The present
 CC sequence represents a cDNA encoding a fragment of gene encoding human
 CC membrane-associated proteins, receptors or ion channels.

XX Sequence 948 BP; 291 A; 171 C; 194 G; 292 T; 0 other;

Query Match 3.1%; Score 19; DB 25; Length 948;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 261 AGCTATTATTGATGCCA 279
 |||||
 DB 678 AGCTATTATTGATGCCA 696

RESULT 13

AAA98873/C
 ID AAA98873 standard; cDNA, 989 BP.

AC AAA98873;

DT 16-FEB-2001 (first entry)

DE Human proliferation-associated endothelial EST cDNA SEQ ID NO 18.

XX EST; expressed sequence tag; human; cell differentiation; antidiabetic;
 KW cell proliferation; endothelial tissue; angiogenic; antiproliferative;
 KW ophthalmological; nephrotropic; cytosolic; hepatotropic; antiarthritic;
 KW antiarteriosclerotic; antirheumatic; gene therapy; angiogenic disease;
 KW treatment; rheumatoid arthritis; haemangioma; angiodiroma; eye disease;
 KW diabetic retinopathy; glaucoma; kidney disease; glomerulonephritis;
 KW diabetic nephropathy; malign nephrosclerosis; transplant rejection;
 KW thrombotic microangiopathic syndrome; glomerulopathy; fibrotic disease;
 KW mesangial cell proliferative disease; ss.

XX Homo sapiens.

OS Homo sapiens.

PN DE19911684-A1.

XX 14-SEP-2000.

XX 09-MAR-1999; 99DE-1011684.

XX 09-MAR-1999; 99DE-1011684.

XX (SCHD) SCHERING AG.

XX Glienke J, Thierauch K, Hinzmann B, Pilarsky C;

DR WPI; 2000-588417/56.

XX Human nucleic acid sequences from endothelial cells useful for
 PT treatment of angiogenic disease, including psoriasis, arthritis and
 PT diabetic retinopathy, etc -
 XX Claim 1a; Page 75-76; 84pp; German.

XX This invention describes novel human nucleic acid sequences (I) from
 CC endothelial cells which have angiogenic, antiproliferative, antidiabetic,
 CC ophthalmological, nephrotropic, cytosolic, hepatotropic,
 CC antiarteriosclerotic, antiarthritic, antirheumatic activity and can be
 CC used for gene therapy. The nucleic acid sequences may find use as tools
 CC to identify agents against angiogenic diseases. The polypeptides may be
 CC used in medicaments for gene therapy to treat angiogenic diseases. (I)
 CC in sense or antisense form may be used. The genomic genes may also be
 CC used with suitable promoters and/or enhancers. The sequences (nucleic
 CC acid and proteins) may be used to treat psoriasis, arthritis, especially
 CC rheumatoid arthritis, haemangioma, angiodiroma, eye diseases, especially
 CC diabetic retinopathy, neovascular glaucoma, kidney disease, such as
 CC glomerulonephritis, diabetic nephropathy, malign nephrosclerosis,
 CC thrombotic microangiopathic syndrome, transplant rejection and
 CC glomerulopathy, fibrotic disease, such as liver cirrhosis, mesangial cell
 CC proliferative disease, arteriosclerosis and injury to nerve tissue.

XX Sequence 989 BP; 261 A; 246 C; 183 G; 299 T; 0 other;

Query Match 3.1%; Score 19; DB 21; Length 989;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 282 ATTACTTTTATGCTGTT 300
 |||||
 DB 771 ATTACTTTTATGCTGTT 753

RESULT 14

AAA98155/C
 ID AAA98155 standard; cDNA, 989 BP.

AC AAA98155;

DT 26-JAN-2001 (first entry)

DE Human proliferation-associated protein EST encoded cDNA #17.

XX Proliferation-associated protein; differentiation-associated protein;
 KW EST; expressed sequence tag; endothelial cell; anti-angiogenic;
 KW angiogenic; antiproliferative; anti-arthritic; antifibrotic; hepatotropic;
 KW antiarteriosclerotic; nephrotropic; antidiabetic; ophthalmological;
 KW immunosuppressive; neuroprotective; gene therapy; psoriasis; arthritis;
 KW hemangioma; diabetic retinopathy; glomerulonephritis; liver cirrhosis;
 KW transplant rejection; arteriosclerosis; nervous tissue injury; human; ss.

OS Homo sapiens.

PN WO200053734-A2.

XX 14-SEP-2000.

XX 08-MAR-2000; 2000WO-EP02005.

XX 09-MAR-1999; 99DE-1011684.

XX 01-OCT-1999; 99DE-1048679.

XX (SCHD) SCHERING AG.

XX Thierauch K, Glienke J, Hinzmann B, Pilarsky C;

XX WPI; 2000-572267/53.

XX Nucleic acid sequences from human endothelial cells, useful for gene
 PT therapy of angiogenesis and for identifying antiangiogenic agents -

XX Claim 1a; Page 107-108; 115pp; German.
PS
XX
CC This invention describes novel nucleic acid sequence (I) obtained from
CC an endothelial cell comprising any of 59 sequences (defined and given in
CC the specification), its allelic variant, or complement. The products of
CC the invention have anti-angiogenic, angiogenic, antiproliferative,
CC anti-atheritic, antifibrotic, antiarteriosclerotic, nephrotropic,
CC antidiabetic, ophthalmological, hepatotropic, immunosuppressive and
CC neuroprotective activity. (I) are implicated in differentiation and
CC proliferation of endothelial cells. (I) are used for expression of
CC polypeptides (IV) that are useful for identifying agents (A) for
CC treatment of angiogenic disease, to express (IV) from gene therapy
CC vectors for treatment of such diseases and as antisense reagents. (IV)
CC are also used to raise specific antibodies. Angiogenic diseases that
CC may be treated include psoriasis, arthritis, hemangioma, diabetic
CC retinopathy, glomerulonephritis, transplant rejection, liver cirrhosis,
CC arteriosclerosis and injuries to nervous tissue. AA98102-A98161
CC represent proliferation-associated and differentiation-associated EST
CC (expressed sequence tag) derived sequences which are described in the
CC method of the invention.
CC
SQ Sequence 989 BP; 261 A; 246 C; 183 G; 299 T; 0 other;
Query Match 3.1%; Score 19; DB 21; Length 989;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 282 ATTACTTTTATGCTGTT 300
Db 771 ATTACTTTTATGCTGTT 753
RESULT 15
AAD29984/C
ID AAD29984 standard; DNA; 989 BP.
XX
AC AAD29984;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human pharmaceutical compound #53 for cancer treatment.
XX
KW Human; pharmaceutical composition; compound I; tumour; psoriasis; cancer;
KW rheumatoid arthritis; vascular endothelial growth factor; VEGF; therapy;
KW neovascular glaucoma; compound II; angiopoietin/Tie receptor system;
KW retinopathy; glomerulonephritis; diabetic nephropathy; nephrosclerosis;
KW thrombotic microangiopathic syndrome; transplantation; glomerulopathy;
KW fibrotic disease; cirrhotic liver; proliferative disease; nephrotropic;
KW ophthalmological; arteriosclerosis; cytostatic; hepatotropic; oedema; ds.
XX
OS Homo sapiens.
XX
PN WO200197850-A2.
XX
PD 27-DEC-2001.
XX
PF 20-JUN-2001; 2001WO-EP06976.
XX
PR 23-JUN-2000; 2000EP-0250194.
PR 28-JUN-2000; 2000EP-0250214.
XX
PA (SCHD) SCHERING AG.
PA (SIEM) SIEMENS G.
PA (HABE/) HABEREY M.
PA (THIE/) THIERAUCH K.
XX
PI Siemeister G, Haberey M, Thierauch K;
XX
DR WPI; 2002-179543/23.
XX
PT Novel composition useful for treating cancer, comprises agents
interfering with vascular endothelial growth factor/VEGF receptor

PT system activity and agents interfering with Angiopoietin/Tie receptor
PT system function -
XX
PS Claim 12; Page 76-77; 79pp; English.
XX
CC The present invention relates to a pharmaceutical composition comprising
CC a combination of substances (compound I) interfering with the biological
CC activity of vascular endothelial growth factor (VEGF)/VEGF receptor
CC systems and substances (compound II) interfering with the biological
CC function of angiotensin/Tie receptor systems. The pharmaceutical
CC composition is useful for the production of a medicament for the
CC treatment of tumours, cancers, psoriasis, arthritis, such as rheumatoid
CC arthritis, haemangioma, angiodioma, eye disease such as diabetic
CC retinopathy, neovascular glaucoma, kidney disease such as
CC glomerulonephritis, diabetic nephropathy, malignant nephrosclerosis,
CC thrombotic microangiopathic syndrome, transplantation rejections and
CC glomerulopathy, fibrotic disease such as cirrhotic liver, mesangial cell
CC proliferative diseases, arteriosclerosis, damage of nerve tissues,
CC suppression of the ascites formation in patients and suppression of VEGF
CC oedemas. The present sequence is human pharmaceutical compound used in
CC the invention.
CC
SQ Sequence 989 BP; 261 A; 246 C; 183 G; 299 T; 0 other;
Query Match 3.1%; Score 19; DB 24; Length 989;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 282 ATTACTTTTATGCTGTT 300
Db 771 ATTACTTTTATGCTGTT 753
RESULT 16
AAL26601/C
ID AAL26601 standard; cDNA; 1061 BP.
XX
AC AAL26601;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 19058.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI; 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS Claim 1; Page 3590; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
(AAL07544-AAL26789) and methods of assessing whether a patient is

CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.

XX
SQ Sequence 1061 BP; 355 A; 170 C; 202 G; 319 T; 15 other;

Query Match 3.1%; Score 19; DB 22; Length 1061;
Best Local Similarity 100.0%; Pred.No. 37;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 372 TAAATTAATATATATAAA 390
|||||

Db 802 TAAATTAATATATATAAA 784
|||||

RESULT 17
AAN71064

ID AAN71064 standard; DNA; 1908 BP.

XX AAN71064;

DT 25-MAR-2003 (updated)
DT 01-JAN-1980 (first entry)

DE Gene encoding Plasmodium vivax sporozoite circumsporozoite protein.

XX Immunogen; vaccine; malaria; immunodominant epitope; ss.

XX Plasmodium vivax.

XX Key Location/Qualifiers

FT CDS 157..1293

FT FT /tag= a

FT FT /product= circumsporozoite protein

XX W08700533-A.

XX 29-JAN-1987.

XX 24-JUN-1986; 86WO-US01373.

XX 12-JUL-1985; 85US-0754645.

XX 30-MAR-1987; 87US-0032327.

XX (UANY) UNIV NEW YORK STATE.

XX (ARNO/) ARNOT D E.

XX Arnot DE, Enea V, Nussenzwei RS, Nussenzweig V;

XX WPI; 1987-037250/05.

XX P-PSDB; AAP0708.

XX New Plasmodium vivax circumsporozoite protein - and synthetic

XX peptide(s) contg. its dominant epitope, useful in anti-malarial

XX vaccines

XX Disclosure; fig. 3; 32pp; English.

XX This circumsporozoite protein of P. vivax sporozoites encoded by

XX this gene is useful in the construction of an anti-malarial

XX vaccine. The sequence consists of a central domain of AAP0704

XX repeated 19 times plus N- and C-terminal regions (practically

XX homologous with the corresponding domains of P. cynomolgi and P.

XX knowlesi. See also AAP0704-07, AAP0709 and AAN71065.

XX (Updated on 25-MAR-2003 to correct PR field.)

XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1908 BP; 677 A; 353 C; 470 G; 408 T; 0 other;

Query Match 3.1%; Score 19; DB 8; Length 1908;
Best Local Similarity 100.0%; Pred.No. 36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 TAAATTAATGAGTAA 375
|||||

Db 251 TAAATTAATGAGTAA 269
|||||

RESULT 18
AAS30510

ID AAS30510 standard; DNA; 2422 BP.

XX AAS30510;

DT 21-NOV-2001 (first entry)

DE DNA encoding novel prostate gland antigen, Seq ID No 368.

XX Human; noctropic; cytoprotective; cytostatic; antiparkinsonian;

XX antianemic; dermatological; immunosuppressive; antiinflammatory;

XX antianthratic; antineumatic; virucide; hepatotropic; nephrotropic;

XX osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss;

XX hyperplasia; carcinoma; prostate neoplastic disorder; skin aging;

XX reproductive system disorder; autoimmune disorder; urinary system;

XX systemic lupus erythematosus; rheumatoid arthritis; cardiovascular;

XX blood-related disorder; hyperproliferative disorder; respiratory;

XX neurological disorder; endocrine disorder; inflammatory disorder;

XX liver disorder; wound healing; food preservative; ds.

XX Homo sapiens.

XX WO200155447-A1.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01330.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220963.

XX 26-JUL-2000; 2000US-0220964.

XX 14-AUG-2000; 2000US-0224518.

XX 14-AUG-2000; 2000US-0224519.

XX 14-AUG-2000; 2000US-0225213.

XX 14-AUG-2000; 2000US-0225214.

XX 14-AUG-2000; 2000US-0225266.

XX 14-AUG-2000; 2000US-0225267.

XX 14-AUG-2000; 2000US-0225268.

XX 14-AUG-2000; 2000US-0225270.

XX 14-AUG-2000; 2000US-0225447.

XX 14-AUG-2000; 2000US-0225757.

XX 14-AUG-2000; 2000US-0225758.

XX 14-AUG-2000; 2000US-0225759.

XX 18-AUG-2000; 2000US-0226279.

XX 22-AUG-2000; 2000US-0226681.

XX 22-AUG-2000; 2000US-0226868.

XX 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 06-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
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 (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-476223/51.
 XX Novel isolated prostate gland related polypeptide useful for diagnosis
 XX and treatment of disorders of prostate such as prostatodytonia,
 XX prostatic hyperplasia, benign prostatic hypertrophy and malacoplakia
 PT
 PS Claim 1; SEQ ID No 368; 512pp; English.
 XX
 XX The invention relates to novel isolated prostate gland related nucleic
 XX acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis,
 XX prognosis, prevention, and/or treatment of diseases and/or disorders of
 XX the prostate such as acute non-bacterial prostatitis, chronic non-
 XX bacterial prostatitis, acute bacterial prostatitis, prostatodystonia,
 XX prostatic hyperplasia, benign prostatic hyperplasia, benign prostatic
 XX adenocarcinoma, transitional cell carcinoma, ductal carcinoma, and
 XX squamous cell carcinoma. (I), (II) and antibody to (II) are useful for
 XX diagnosing and treating reproductive system disorders (Paget's disease),
 XX autoimmune disorders (systemic lupus erythematosus, rheumatoid
 XX arthritis), blood-related disorders (sickle cell anaemia),
 XX hyperproliferative disorders, urinary system disorders
 XX (glomerulonephritis), cardiovascular disorders (arrhythmias),
 XX respiratory disorders, musculoskeletal system disorders, neural activity
 XX and neurological disorders (Alzheimer's disease and Parkinson's disease),
 XX endocrine disorders (Addison's disease), gastrointestinal disorders
 XX (inflammatory disorders), liver disorders (biliary liver cirrhosis),
 XX pancreatic and gall bladder disorders, disorders of the large intestine,
 XX developmental and inherited disorders, diseases at the cellular level,
 XX and wound healing and epithelial cell proliferation. (I) or (II) is
 XX useful to prevent skin aging, for preventing hair loss, to maintain

Query Match 3.1%; Score 19; DB 22; Length 2422;
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DT 21-NOV-2001 (first entry)
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KW Human; noctropic; neuroprotective; cytosolic; antiparkinsonian;
KW antianaemic; dermatological; immunosuppressive; antiinflammatory;
KW antiarthritic; antineoplastic; virocid; hepatotropic; nephrotropic;
KW osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss;
KW prostatic; malacoplakia; adenocarcinoma; benign prostatic hypertrophy;
KW hyperplasia; carcinoma; prostate neoplastic disorder; skin aging;
KW reproductive system disorder; autoimmune disorder; urinary system;
KW systemic lupus erythematosus; rheumatoid arthritis; cardiovascular;
KW blood-related disorder; hyperproliferative disorder; respiratory;
KW neurological disorder; endocrine disorder; inflammatory disorder;
KW liver disorder; wound healing; food preservative; ds.
XX
OS Homo sapiens.
XX
PN WO200155447-A1.
XX
XX 02-AUG-2001.
XX
PD 17-JAN-2001; 2001WO-US01330.
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XX
XX (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-476223/51.
XX
XX Novel isolated prostate gland related polypeptide useful for diagnosis
PT and treatment of disorders of prostate such as prostatic dysplasia,
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PT
XX
XX Claim 1; SEQ ID No 369; 512pp; English.
XX
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CC acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis,
CC prognosis, prevention, and/or treatment of diseases and/or disorders of
CC the prostate such as acute non-bacterial prostatitis, chronic non-
CC bacterial prostatitis, acute bacterial prostatitis, prostatic dysplasia,
CC prostatic hyperplasia, acute bacterial prostatitis, benign prostatic
CC hyperplasia, granulomatous prostatitis, malacoplakia, benign prostatic
CC hyperplasia, and prostate neoplastic disorders, including
CC adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and
CC squamous cell carcinomas. (I), (II) and antibody to (II) are useful for
CC diagnosing and treating reproductive system disorders (Paget's disease),
CC autoimmune disorders (systemic lupus erythematosus, rheumatoid
CC arthritis), blood-related disorders (sickle cell anaemia),
CC hyperproliferative disorders, urinary system disorders
CC (glomerulonephritis), cardiovascular disorders (arrhythmias),
CC respiratory disorders, musculoskeletal system disorders, neural activity
CC and neurological disorders (Alzheimer's disease and Parkinson's disease),
CC endocrine disorders (Addison's disease), gastrointestinal disorders
CC (inflammatory disorders), liver disorders (biliary liver cirrhosis),
CC pancreatic and gall bladder disorders, disorders of the large intestine,
CC developmental and inherited disorders, diseases at the cellular level,
CC and wound healing and epithelial cell proliferation. (I) or (II) is
CC useful to prevent skin aging, for preventing hair loss, to maintain

XX
DT 21-NOV-2001 (first entry)
XX
XX Human reproductive system related antigen DNA SEQ ID NO: 8977.
DE
XX Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
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OS Homo sapiens.
XX
XX NO200155320-A2.
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PD 02-AUG-2001.
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 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Rosen CA, Barash SC, Ruben SM;
 XX
 PI WPI; 2001-465570/50.
 XX
 DR Isolated nucleic acid molecule encoding a reproductive system antigen
 XX is used in preventing, treating or ameliorating a medical condition -
 PT
 XX
 PS Disclosure: SEQ ID NO 8978; 1297pp + Sequence Listing; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention.
 XX
 SQ Sequence 2422 BP; 743 A; 494 C; 595 G; 590 T; 0 other;
 Query Match 3.1%; Score 19; DB 22; Length 2422;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY . 282 ATTACTTTTATGCTGCTT 300
 DB 1593 ATTACTTTTATGCTGCTT 1611

RESULT 22
 ABX63452
 ID ABX63452 standard; cDNA; 3318 BP.
 XX
 AC ABX63452;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE Human cDNA #452 differentially expressed in activated vascular tissue.
 XX
 KW Human; gene; ss; vascular tissue; cytosolic; atherosclerosis;
 KW cardiatic; hypotensive; antidiabetic; gynaecological; vasotropic;
 KW cerebroprotective; gene therapy; vascular disease; cancer; coronary;
 KW artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
 KW ischaemia-reperfusion injury; stroke;
 XX
 OS Homo sapiens.
 XX
 PN US2002137081-A1.
 XX
 PD 26-SEP-2002.
 XX
 PF 08-JAN-2002; 2002US-0044090.
 XX
 PR 28-JUL-2000; 2000US-222469P.
 PR 08-JAN-2001; 2001US-260483P.
 XX
 PA (BAND/) BANDMAN O.
 XX
 PI Bandman O;
 XX
 DR MPI; 2003-110597/10.
 XX
 PT Combination for diagnosing, staging, treating, or monitoring the
 PT progression of treatment of a vascular disease, e.g. atherosclerosis,
 PT comprises several CDNAs that are differentially expressed in activated
 PT vascular tissue -
 XX
 PS Claim 1; Page -; 18pp; English.
 XX
 CC This invention relates to a combination comprising several CDNAs that
 CC are differentially expressed in activated vascular tissue. The invention
 CC also discloses a high throughput method for detecting differentially
 CC expressed CDNAs in a sample. The CDNAs of the invention may have
 CC antiarteriosclerotic, cytoprotective, cardiatic, hypotensive, antidiabetic;
 CC gynaecological, vasotropic and cerebroprotective activities and may be
 CC used in gene therapy. The CDNAs of the invention may be used in a
 CC high-throughput methods for detecting differential expression of one or
 CC more CDNAs in a sample, or screening several molecules or compounds to
 CC identify a molecule or compound that specifically binds a cDNA of the
 CC invention. A protein encoded by the cDNA may be used to screen several
 CC molecules or compounds to identify a ligand that specifically binds to
 CC the protein, or to produce or purify an antibody to the protein that can
 CC be used to detect a protein in a sample or purify a natural or
 CC recombinant protein from a sample. The nucleotides may be useful for
 CC diagnosing, staging, treating, or monitoring the progression of
 CC treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary
 CC artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-
 CC reperfusion injury, restenosis, or stroke. The CDNAs can also be used
 CC for large-scale genetic or gene expression analysis of several new
 CC nucleic acid molecules. Antibodies to the proteins encoded by the
 CC CDNAs are useful for diagnosing pre-pathologic disorders, and chronic
 CC or acute diseases associated with abnormalities in the expression,
 CC amount or distribution of the protein. The present sequence
 CC represents a cDNA of the invention that is differentially expressed in
 CC activated vascular tissue.
 CC Note: The sequence data for this patent did not form part of the
 CC specification, but was obtained in electronic format directly from USPTO
 CC at <http://seqdata.uspto.gov/sequence.html?docID=20020137081>.
 XX
 SQ Sequence 3318 BP; 1029 A; 566 C; 628 G; 1093 T; 2 other;

Query Match 3.1%; Score 19; DB 25; Length 3318;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 261 ACCTATTTTATGATGCCA 279
 |||||
 DB 1507 AGCTATTTTATGATGCCA 1525
 |||||
 RESULT 23
 ABL15016
 ID ABL15016 standard; cDNA; 4357 BP.
 XX
 AC ABL15016;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39530.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEXE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR MPI; 2001-656860/75.
 DR P-PsDB; ABB70913.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 39530; 21pp + Sequence listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABR72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_ptc_sequences.
 XX
 SQ Sequence 4357 BP; 1181 A; 981 C; 970 G; 1225 T; 0 other;
 QY 369 GAGTAAATTATATATATA 387
 |||||
 DB 1486 GAGTAAATTATATATATA 1504
 |||||
 RESULT 24
 ABL26996
 ID ABL26996 standard; DNA; 4466 BP.
 Query Match 3.1%; Score 19; DB 23; Length 4357;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX ABL26996;
AC
XX 26-MAR-2002 (first entry)
DT
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 32461.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW
XX pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI, 2001-656860/75.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT
XX
XX Claim 1; SEQ ID NO 32461; 21pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB12072).
CC
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
CC
XX
XX Sequence 4466 BP; 1268 A; 1044 C; 951 G; 1203 T; 0 other;
SQ
Query Match 3.1%; Score 19; DB 23; Length 4466;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 369 GAGTAAATTTAATATA 387
DB 4375 GAGTAAATTTAATATA 4393

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KW psoriasis; hepatitis; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200279449-A2.
PN
XX
XX 10-OCT-2002.
PD
XX
XX 27-MAR-2002; 2002WO-US09944.
PF
XX
XX 28-MAR-2001; 2001US-279619P.
PR
XX 29-MAR-2001; 2001US-280067P.
PR
XX 29-MAR-2001; 2001US-280068P.
PR
XX 16-MAY-2001; 2001US-291280P.
PR
XX 17-MAY-2001; 2001US-291829P.
PR
XX 17-MAY-2001; 2001US-291849P.
PR
XX 19-JUN-2001; 2001US-299428P.
PR
XX 20-JUN-2001; 2001US-299776P.
PR
XX 20-JUN-2001; 2001US-300001P.
XX
XX (INCY) INCYTE GENOMICS INC.
PA
XX
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;
PI Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleeefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
DR
XX WPI; 2003-058431/05.
DR
XX P-PSDB; AB11526.
XX
XX New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis -
PT
XX
XX Claim 1; SEQ ID NO 77; 339pp + Sequence Listing; English.
PS
XX
XX This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDPT) which has anti-inflammatory, immunosuppressive,
CC osteopoeitic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammatory osteoporosis, thrombocytopenia, psoriasis or
CC hepatitis. ABX34440-ABX34835 encode the MDPT polypeptides represented in
CC AB011450-AB011845, described in the disclosure of the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
XX
XX Sequence 5694 BP; 1558 A; 1155 C; 1210 G; 1771 T; 0 other;
SQ
Query Match 3.1%; Score 19; DB 25; Length 5694;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 261 AGCTATTTTATGATGCCA 279
DB 3924 AGCTATTTTATGATGCCA 3942

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RESULT 25
ABX34516
ID ABX34516 standard; cDNA; 5694 BP.
AC
XX ABX34516;
AC
XX
XX 13-FEB-2003 (first entry)
DT
XX
XX Human mdct cDNA SEQ ID 77.
DE
XX
XX MDDT; human; disease detection and treatment molecule polypeptide;
KW anti-inflammatory; immunosuppressive; osteopoeitic; cytostatic; anti-HIV;
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW gene therapy; protein replacement therapy; cell proliferative disorder;
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopenia;
KW

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RESULT 26
AAV33135/C
ID AAV33135 standard; DNA; 5849 BP.
AC
XX AAV33135;
AC
XX

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PR 14-SEP-2000; 2000US-0234401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0250393.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256711.
 PR 06-DEC-2000; 2000US-0251479.

PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-476223/51.
 XX
 PT Novel isolated prostate gland related polypeptide useful for diagnosis
 PT and treatment of disorders of prostate such as prostatodystonia,
 PT prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
 PT
 XX
 PS Claim 1; SEQ ID No 367; 512pp; English.
 XX
 CC The invention relates to novel isolated prostate gland related nucleic
 CC acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis,
 CC prognosis, prevention, and/or treatment of diseases and/or disorders of
 CC the prostate such as acute non-bacterial prostatitis, chronic non-
 CC bacterial prostatitis, acute bacterial prostatitis, prostatodystonia,
 CC prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic
 CC hypertrophy or hyperplasia, and prostate neoplastic disorders, including
 CC adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and
 CC squamous cell carcinomas. (I), (II) and antibody to (II) are useful for
 CC diagnosing and treating reproductive system disorders (Paget's disease),
 CC autoimmune disorders (systemic lupus erythematosus, rheumatoid
 CC arthritis), blood-related disorders (sickle cell anaemia),
 CC hyperproliferative disorders, urinary system disorders
 CC (glomerulonephritis), cardiovascular disorders (arrhythmias),
 CC respiratory disorders, musculoskeletal system disorders, neural activity
 CC and neurological disorders (Alzheimer's disease and Parkinson's disease),
 CC endocrine disorders (Addison's disease), gastrointestinal disorders
 CC (inflammatory disorders), liver disorders (biliary liver cirrhosis),
 CC pancreatic and gall bladder disorders, disorders of the large intestine,
 CC developmental and inherited disorders, diseases at the cellular level,
 CC and wound healing and epithelial cell proliferation. (I) or (II) is
 CC useful to prevent skin aging, for preventing hair loss, to maintain
 CC
 Query March 3.1%; Score 19; DB 22; Length 10468;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 282 ATTACTTTTATGCTGTT 300
 Db 7435 ATTACTTTTATGCTGTT 7453
 ID AAS30512 standard; DNA; 10468 BP.
 AC AAS30512;
 XX
 DT 21-NOV-2001 (first entry)
 DE DNA encoding novel prostate gland antigen, Seq ID No 370.
 XX
 KW Human; noctropic; neuroprotective; cytosolic; antiparkinsonian;
 KW antihaemic; dermatological; immunosuppressive; antiinflammatory;
 KW antidiabetic; antirheumatic; vitruicide; hepatotropic; nephrotropic;
 KW osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss;
 KW prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy;
 KW hyperplasia; carcinoma; prostate neoplastic disorder; skin aging;
 KW reproductive system disorder; autoimmune disorder; urinary system;
 KW systemic lupus erythematosus; rheumatoid arthritis; cardiovascular;
 KW blood-related disorder; hyperproliferative disorder; respiratory;
 KW neurological disorder; endocrine disorder; inflammatory disorder;

KW liver disorder; wound healing; food preservative; ds.
XX
OS Homo sapiens.
XX
PN MO200155447-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01330.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
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PR 20-OCT-2000; 2000US-0241809.
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PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
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PR 08-DEC-2000; 2000US-0251858.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
PI WPI, 2001-476223/51.
XX
XX Novel isolated prostate gland related polypeptide useful for diagnosis
PT and treatment of disorders of prostate such as prostatic hyperplasia,
PT prostatic hyperplasia, prostatic hyperplasia, benign prostatic hyperplasia and malacoplakia
PT
PS Claim 1, SEQ ID No 370; 512bp; English.
XX
XX The invention relates to novel isolated prostate gland related nucleic
CC acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis,
CC prognosis, prevention, and/or treatment of diseases and/or disorders of
CC the prostate such as acute non-bacterial prostatitis, chronic non-
CC bacterial prostatitis, acute bacterial prostatitis, prostatic hyperplasia,
CC prostatic hyperplasia, prostatic hyperplasia, malacoplakia, benign prostatic
CC hyperplasia or hyperplasia, and prostate neoplastic disorders, including
CC adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and
CC squamous cell carcinomas. (I), (II) and antibody to (II) are useful for
CC diagnosing and treating reproductive system disorders (Paget's disease),
CC autoimmune disorders (systemic lupus erythematosus, rheumatoid
CC arthritis), blood-related disorders (sickle cell anaemia),
CC hyperproliferative disorders, urinary system disorders
CC (glomerulonephritis), cardiovascular disorders (arrhythmias),
CC respiratory disorders, musculoskeletal system disorders, neural activity
CC and neurological disorders (Alzheimer's disease and Parkinson's disease),
CC endocrine disorders (Addison's disease), gastrointestinal disorders
CC (inflammatory disorders), liver disorders (biliary liver cirrhosis),
CC pancreatic and gall bladder disorders, disorders of the large intestine,
CC developmental and inherited disorders, diseases at the cellular level,
CC and wound healing and epithelial cell proliferation. (I) or (II) is
CC useful to prevent skin aging, for preventing hair loss, to maintain

Query Match 3.1%; Score 19; DB 22; Length 10468;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 ATTACTTTTATGCTGTT 300
Db 7435 ATTACTTTTATGCTGTT 7453
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XX
DT 21-NOV-2001 (first entry)
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XX Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
XX WO200155320-A2.
XX
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XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01339.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
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PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI
XX
XX Rosen CA, Barash SC, Ruben SM;
DR WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
PS Disclosure; SEQ ID NO 8976; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a

CC protein of the invention.
XX
SQ Sequence 10468 BP; 2791 A; 2285 C; 2566 G; 2826 T; 0 other;
Query Match 3.1%; Score 19; DB 22; Length 10468;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 282 ATTACTTTTATTGCTGTT 300
DB 7435 ATTACTTTTATTGCTGTT 7453
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XX
XX AAL06291;
AC
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 8979.
XX
XX Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
XX WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
XX
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 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-465570/50.
 DR
 XX
 XX
 PT Isolated nucleic acid molecule encoding a reproductive system antigen
 PT is used in preventing, treating or ameliorating a medical condition -
 XX
 PS Disclosure; SEQ ID NO 8979; 1297bp + Sequence Listing; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention.
 XX
 SQ Sequence 10468 BP; 2791 A; 2285 C; 2566 G; 2826 T; 0 other;
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 Db 282 ATTACTTTTATGCTGTT 300
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 DT 28-AUG-2002 (first entry)
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 DE Human angiogenesis associated polynucleotide SEQ ID NO 27.
 KW Human; angiogenesis; methylation; eye disease; glaucoma; tumour;
 KW inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds;
 KW macular degeneration; inflammatory bowel disease; Crohn's disease;
 KW antihypertensive; antiarrhythmic; antidiabetic; antipsoriatic;
 XX
 OS Homo sapiens.
 XX
 PN WO200246454-A2.
 XX

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PD 13-JUN-2002.
XX
XX 06-DEC-2001; 2001WO-EP14320.
XX
XX 06-DEC-2000; 2000DE-1061338.
XX
XX (EP1G-) EPIGENOMICS AG.
XX
XX Schacht O;
XX
XX WPI; 2002-500450/53.
XX
XX New nucleic acid fragments from chemically treated
XX angiogenesis-associated genes, useful for determining methylation
XX status, e.g. in diagnosis or treatment of cancer -
XX
XX Claim 1; SEQ ID NO 27; 41pp + Sequence listing; German.
XX
XX The invention relates to a nucleic acid (I) comprising a segment of 18
XX bases of chemically pretreated DNA of angiogenesis-associated genes (II)
XX having sequences (AB066971-AB067178) or their complements. (I), also
XX related oligomers, are used to evaluate the methylation status and/or
XX single-nucleotide polymorphisms, in angiogenesis-related genes, for
XX diagnosis and treatment of eye diseases, proliferative retinopathy,
XX neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis,
XX diabetic retinopathy, macular degeneration caused by neovascularisation,
XX psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and
XX Crohn's disease.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
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KW gene therapy; atopic disorder; non-Hodgkin's lymphoma;
KW Hodgkin's lymphoma; allergic disease; gene; ss; chromosome 11q12-13.1.
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XX
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FT /tag= d
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FT intron 43080..43667
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FT /tag= l
FT /number= 6
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FT WO200262946-A2.
XX
XX 15-AUG-2002.
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XX 10-DEC-2001; 2001WO-US48437.
XX
XX 08-DEC-2000; 2000US-254362P.
XX 20-FEB-2001; 2001US-270057P.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Tedder TF, Liang YH;
XX
XX WPI; 2002-657530/70.
XX
XX New membrane spanning 4-domain A (MS4A) genes and polypeptides, useful
XX for generating animal models of atopic disorders, for drug screening,
XX or for treating (non-) Hodgkin's lymphoma, or allergic or atopic
XX disorders in e.g. humans -
XX
XX Claim 18; Page 227-255; 450pp; English.
XX
XX The invention relates to novel membrane spanning 4-domain A (MS4A)
XX nucleic acid and polypeptide molecules, comprising human and mouse
XX The polypeptides of the invention have cytosstatic and antiallergic
XX activity. The polynucleotides may have a use in gene therapy. The MS4A
XX nucleic acids and polypeptides are useful for generating animal (e.g.
XX mouse) models of atopic disorders, or for drug discovery screens. These
XX are also useful for treating (non-)Hodgkin's lymphoma, allergic
XX diseases, atopic disorders or other MS4A-related conditions. The present
XX sequence represents a human MS4A genomic region.
XX
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SQ
Query Match 3.1%; Score 19; DB 24; Length 51959;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DT 26-SEP-2001 (first entry)
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KM Corynebacterium; amino acid synthesis; vitamin; saccharide;
KM organic acid synthesis; ds.
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PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-0127688.
XX
PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
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PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
XX
PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT
PS Disclosure; SEQ ID NO: 7064; 246bp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of corynebacterium bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
CC from corynebacterium bacterium. Corynebacterium bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
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Best Local Similarity 100.0%; Pred. No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 335974 TTTAATATATATAAAGGCT 335992

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AC AAH68530;
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DT 26-SEP-2001 (first entry)
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DE C glutamicum coding sequence fragment SEQ ID NO: 7065.
XX

KM Corynebacterium; amino acid synthesis; vitamin; saccharide;
KM organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-0127688.
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PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
XX
PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT
PS Disclosure; SEQ ID NO: 7065; 246bp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of corynebacterium bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
CC from corynebacterium bacterium. Corynebacterium bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
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SQ Sequence 349980 BP; 86896 A; 98023 C; 80939 G; 84122 T; 0 other;
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DT 16-OCT-2001 (first entry)
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KM SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;
KM 240017 region G3; 318013 region A3; 515002 region G2; ds.
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PN WO200151627-A2.
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PD 19-JUL-2001.


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XX AC ABT01503;
XX DT 07-NOV-2002 (first entry)
XX DE Human neuregulin 1 gene.
XX KW Human; neuregulin 1; neuregulin-1-associated gene 1; NRG1; NRG1AG1;
XX KW schizophrenia; chromosome 8p12; single nucleotide polymorphism; SNP;
XX KW neuroleptic; gene therapy; gene; ds.
XX OS Homo sapiens.
XX FH Key
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disorders associated with decreased neuregulin 1 expression by rectifying mutations or deletions in a patient's genome that affect the activity of neuregulin 1 by expressing inactive proteins or to supplement the patients own production of polypeptides. Additionally, the gene may be used to produce the neuregulin 1 protein, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The gene and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The protein may also be used as antigens in the production of antibodies against neuregulin 1 and in assays to identify modulators of neuregulin 1 expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of neuregulin 1 in samples.

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Job time : 257 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 06:23:16 ; Search time 57 Seconds
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4816.497 Million cell updates/sec

Title: US-10-010-160-1
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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| 29 | 17 | 2.7 | 4053 | 4 | US-09-620-312D-156 | Sequence 156, App |
| 30 | 17 | 2.7 | 5561 | 2 | US-08-400-159-1 | Sequence 1, Appli |
| 31 | 17 | 2.7 | 5561 | 3 | US-08-611-729A-1 | Sequence 1, Appli |
| 32 | 17 | 2.7 | 6846 | 4 | US-08-961-527-198 | Sequence 198, App |
| 33 | 17 | 2.7 | 7573 | 4 | US-08-287-959-2 | Sequence 2, Appli |
| 34 | 17 | 2.7 | 90541 | 4 | US-09-759-359A-3 | Sequence 3, Appli |
| 35 | 17 | 2.7 | 99500 | 4 | US-09-798-096-10 | Sequence 10, Appli |
| 36 | 17 | 2.7 | 129908 | 4 | US-09-585-858-1 | Sequence 1, Appli |
| 37 | 17 | 2.7 | 1830121 | 4 | US-09-557-884-1 | Sequence 1, Appli |
| 38 | 17 | 2.7 | 1830121 | 4 | US-09-643-990A-1 | Sequence 1, Appli |
| 39 | 16 | 2.6 | 21 | 1 | US-08-290-937B-7 | Sequence 7, Appli |
| 40 | 16 | 2.6 | 44 | 3 | US-08-552-369-3 | Sequence 3, Appli |
| 41 | 16 | 2.6 | 201 | 4 | US-09-134-001C-2767 | Sequence 2767, Ap |
| 42 | 16 | 2.6 | 225 | 4 | US-09-328-352-2277 | Sequence 2277, Ap |
| 43 | 16 | 2.6 | 457 | 4 | US-09-643-597-306 | Sequence 306, App |
| 44 | 16 | 2.6 | 457 | 4 | US-09-480-884A-306 | Sequence 306, App |
| 45 | 16 | 2.6 | 457 | 4 | US-09-542-615A-306 | Sequence 306, App |
| 46 | 16 | 2.6 | 457 | 4 | US-09-606-421B-306 | Sequence 306, App |
| 47 | 16 | 2.6 | 615 | 4 | US-09-291-922-17 | Sequence 17, Appli |
| 48 | 16 | 2.6 | 696 | 4 | US-09-134-001C-2170 | Sequence 2170, Ap |
| 49 | 16 | 2.6 | 708 | 4 | US-09-107-532A-2113 | Sequence 2113, Ap |
| 50 | 16 | 2.6 | 771 | 4 | US-09-328-352-3448 | Sequence 3448, Ap |
| 51 | 16 | 2.6 | 816 | 4 | US-09-328-352-743 | Sequence 443, App |
| 52 | 16 | 2.6 | 873 | 4 | US-08-484-841A-7 | Sequence 7, Appli |
| 53 | 16 | 2.6 | 874 | 3 | US-08-881-450A-24 | Sequence 24, Appli |
| 54 | 16 | 2.6 | 929 | 4 | US-09-452-239-19 | Sequence 19, Appli |
| 55 | 16 | 2.6 | 962 | 4 | US-09-452-239-23 | Sequence 23, Appli |
| 56 | 16 | 2.6 | 960 | 4 | US-09-452-239-21 | Sequence 21, Appli |
| 57 | 16 | 2.6 | 984 | 4 | US-09-328-352-2306 | Sequence 2306, Ap |
| 58 | 16 | 2.6 | 1001 | 4 | US-09-671-317-446 | Sequence 446, App |
| 59 | 16 | 2.6 | 1023 | 4 | US-09-452-239-25 | Sequence 25, Appli |
| 60 | 16 | 2.6 | 1236 | 4 | US-09-918-686-19 | Sequence 19, Appli |
| 61 | 16 | 2.6 | 1407 | 4 | US-09-107-532A-1650 | Sequence 1650, Ap |
| 62 | 16 | 2.6 | 1591 | 4 | US-09-356-806-44 | Sequence 44, Appli |
| 63 | 16 | 2.6 | 1632 | 4 | US-09-600-991-3 | Sequence 3, Appli |
| 64 | 16 | 2.6 | 1709 | 4 | US-09-600-991-21 | Sequence 21, Appli |
| 65 | 16 | 2.6 | 1755 | 4 | US-09-600-991-1 | Sequence 1, Appli |
| 66 | 16 | 2.6 | 1759 | 4 | US-09-600-991-22 | Sequence 22, Appli |
| 67 | 16 | 2.6 | 2017 | 4 | US-09-291-922-21 | Sequence 21, Appli |
| 68 | 16 | 2.6 | 2100 | 4 | US-09-620-312D-542 | Sequence 542, App |
| 69 | 16 | 2.6 | 2172 | 3 | US-08-030-410-2 | Sequence 2, Appli |
| 70 | 16 | 2.6 | 2172 | 4 | US-09-600-991-17 | Sequence 17, Appli |
| 71 | 16 | 2.6 | 2184 | 1 | US-07-815-333A-1 | Sequence 1, Appli |
| 72 | 16 | 2.6 | 2233 | 1 | US-09-484-970B-141 | Sequence 141, App |
| 73 | 16 | 2.6 | 2288 | 1 | US-08-290-937B-4 | Sequence 4, Appli |
| 74 | 16 | 2.6 | 2289 | 1 | US-07-838-410-2 | Sequence 2, Appli |
| 75 | 16 | 2.6 | 2741 | 2 | US-08-832-883-59 | Sequence 59, Appli |
| 76 | 16 | 2.6 | 2741 | 2 | US-08-832-877-59 | Sequence 59, Appli |
| 77 | 16 | 2.6 | 2818 | 3 | US-08-982-493-7 | Sequence 7, Appli |
| 78 | 16 | 2.6 | 2818 | 3 | US-08-628-655-1 | Sequence 1, Appli |
| 79 | 16 | 2.6 | 3942 | 4 | US-09-601-198-50 | Sequence 50, Appli |
| 80 | 16 | 2.6 | 5099 | 4 | US-09-610-040-5 | Sequence 5, Appli |
| 81 | 16 | 2.6 | 7587 | 3 | US-08-378-313-22 | Sequence 22, Appli |
| 82 | 16 | 2.6 | 17656 | 4 | US-09-433-579-3 | Sequence 3, Appli |
| 83 | 16 | 2.6 | 20598 | 4 | US-09-593-995-10 | Sequence 10, Appli |
| 84 | 16 | 2.6 | 26016 | 4 | US-09-326-480A-1 | Sequence 1, Appli |
| 85 | 16 | 2.6 | 28001 | 4 | US-09-819-993-3 | Sequence 3, Appli |
| 86 | 16 | 2.6 | 36741 | 3 | US-09-301-665-3 | Sequence 3, Appli |
| 87 | 16 | 2.6 | 40328 | 3 | US-08-742-185-102 | Sequence 102, App |
| 88 | 16 | 2.6 | 43795 | 3 | US-08-742-185-101 | Sequence 101, App |
| 89 | 16 | 2.6 | 51719 | 4 | US-09-918-686-2 | Sequence 2, Appli |
| 90 | 16 | 2.6 | 58407 | 4 | US-08-916-421B-2 | Sequence 2, Appli |
| 91 | 16 | 2.6 | 74962 | 4 | US-09-685-853A-3 | Sequence 3, Appli |
| 92 | 16 | 2.6 | 74962 | 4 | US-08-685-853A-3 | Sequence 3, Appli |
| 93 | 16 | 2.6 | 79139 | 4 | US-09-918-686-1 | Sequence 1, Appli |
| 94 | 16 | 2.6 | 921005 | 4 | US-09-734-674-3 | Sequence 3, Appli |
| 95 | 16 | 2.6 | 1230025 | 4 | US-09-198-445A-1 | Sequence 1, Appli |
| 96 | 16 | 2.6 | 1664976 | 4 | US-08-916-421B-1 | Sequence 1, Appli |
| 97 | 16 | 2.6 | 1664976 | 4 | US-08-916-421B-1 | Sequence 1, Appli |
| 98 | 16 | 2.6 | 1830121 | 4 | US-09-557-884-1 | Sequence 1, Appli |
| 99 | 16 | 2.6 | 1830121 | 4 | US-09-643-990A-1 | Sequence 1, Appli |
| 100 | 15 | 2.4 | 183 | 4 | US-09-107-532A-2453 | Sequence 2453, Ap |

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|-------|----|-----|------|---|---------------------|--------------------|-------|----|-----|------|---|---------------------|--------------------|
| 101 | 15 | 2.4 | 219 | 4 | US-09-107-532A-2524 | Sequence 2524, Ap | C 174 | 15 | 2.4 | 1651 | 3 | US-09-362-473-1 | Sequence 1, Appl1 |
| C 102 | 15 | 2.4 | 252 | 4 | US-09-328-352-2763 | Sequence 2763, Ap | 175 | 15 | 2.4 | 1662 | 4 | US-09-738-894A-1 | Sequence 1, Appl1 |
| C 103 | 15 | 2.4 | 259 | 4 | US-09-313-294A-2378 | Sequence 2378, Ap | 176 | 15 | 2.4 | 1662 | 4 | US-09-802-117-1 | Sequence 1, Appl1 |
| C 104 | 15 | 2.4 | 277 | 4 | US-09-313-294A-1780 | Sequence 1780, Ap | 177 | 15 | 2.4 | 1662 | 4 | US-09-964-469-1 | Sequence 1, Appl1 |
| C 105 | 15 | 2.4 | 278 | 4 | US-09-313-294A-4575 | Sequence 4575, Ap | 178 | 15 | 2.4 | 1668 | 4 | US-09-107-532A-2768 | Sequence 2, Appl1 |
| C 106 | 15 | 2.4 | 321 | 4 | US-09-702-705-1500 | Sequence 1500, Ap | 179 | 15 | 2.4 | 1669 | 2 | US-08-916-902A-2 | Sequence 2, Appl1 |
| C 107 | 15 | 2.4 | 321 | 4 | US-09-736-457-1500 | Sequence 1500, Ap | 180 | 15 | 2.4 | 1669 | 2 | US-09-213-389-2 | Sequence 2, Appl1 |
| C 108 | 15 | 2.4 | 422 | 4 | US-09-641-638-327 | Sequence 327, Ap | 181 | 15 | 2.4 | 1674 | 2 | US-08-793-410-31 | Sequence 31, Appl1 |
| C 109 | 15 | 2.4 | 422 | 4 | US-09-641-638-328 | Sequence 328, Ap | 182 | 15 | 2.4 | 1700 | 1 | US-08-533-304A-3 | Sequence 3, Appl1 |
| C 110 | 15 | 2.4 | 429 | 1 | US-07-710-361-6 | Sequence 6, Appl1 | 183 | 15 | 2.4 | 1708 | 4 | US-09-620-312D-275 | Sequence 275, Ap |
| C 111 | 15 | 2.4 | 447 | 1 | US-08-211-942-4 | Sequence 4, Appl1 | 184 | 15 | 2.4 | 1733 | 3 | US-09-147-522-1 | Sequence 1, Appl1 |
| C 112 | 15 | 2.4 | 451 | 4 | US-09-322-575-107 | Sequence 107, Ap | 185 | 15 | 2.4 | 1743 | 4 | US-09-134-001C-2774 | Sequence 2774, Ap |
| C 113 | 15 | 2.4 | 451 | 4 | US-09-389-681-107 | Sequence 107, Ap | 186 | 15 | 2.4 | 1761 | 4 | US-09-369-247-21 | Sequence 21, Appl1 |
| C 114 | 15 | 2.4 | 451 | 4 | US-09-620-405B-107 | Sequence 107, Ap | 187 | 15 | 2.4 | 1896 | 4 | US-09-134-001C-1768 | Sequence 1768, Ap |
| C 115 | 15 | 2.4 | 451 | 4 | US-09-339-338-107 | Sequence 107, Ap | 188 | 15 | 2.4 | 1981 | 3 | US-08-981-392-26 | Sequence 26, Appl1 |
| C 116 | 15 | 2.4 | 451 | 4 | US-09-433-825B-107 | Sequence 107, Ap | 189 | 15 | 2.4 | 1995 | 4 | US-09-328-352-2067 | Sequence 2067, Ap |
| C 117 | 15 | 2.4 | 451 | 4 | US-09-604-287A-107 | Sequence 107, Ap | 190 | 15 | 2.4 | 2061 | 2 | US-08-833-170-1 | Sequence 1, Appl1 |
| C 118 | 15 | 2.4 | 464 | 4 | US-09-702-705-3 | Sequence 3, Appl1 | 191 | 15 | 2.4 | 2061 | 3 | US-09-359-257-1 | Sequence 1, Appl1 |
| C 119 | 15 | 2.4 | 464 | 4 | US-09-736-457-3 | Sequence 3, Appl1 | 192 | 15 | 2.4 | 2061 | 4 | US-09-371-674-1 | Sequence 1, Appl1 |
| C 120 | 15 | 2.4 | 513 | 4 | US-09-328-352-1072 | Sequence 1072, Ap | 193 | 15 | 2.4 | 2064 | 3 | US-08-875-944B-1 | Sequence 1, Appl1 |
| C 121 | 15 | 2.4 | 513 | 4 | US-09-328-352-3354 | Sequence 3354, Ap | 194 | 15 | 2.4 | 2064 | 3 | US-09-116-049-3 | Sequence 3, Appl1 |
| C 122 | 15 | 2.4 | 528 | 4 | US-09-328-352-3354 | Sequence 3354, Ap | 195 | 15 | 2.4 | 2064 | 4 | US-09-602-868A-1 | Sequence 1, Appl1 |
| C 123 | 15 | 2.4 | 585 | 3 | US-09-404-671-3 | Sequence 457, Ap | 196 | 15 | 2.4 | 2064 | 4 | US-09-884-363-3 | Sequence 3, Appl1 |
| C 124 | 15 | 2.4 | 621 | 3 | US-09-385-982-180 | Sequence 180, Ap | 197 | 15 | 2.4 | 2130 | 4 | US-09-620-312D-145 | Sequence 145, Ap |
| C 125 | 15 | 2.4 | 623 | 1 | US-08-784-289-2 | Sequence 2, Appl1 | 198 | 15 | 2.4 | 2157 | 4 | US-09-328-352-968 | Sequence 968, Ap |
| C 126 | 15 | 2.4 | 676 | 4 | US-08-747-562-10 | Sequence 10, Appl1 | 199 | 15 | 2.4 | 2168 | 3 | US-08-749-592-6 | Sequence 6, Appl1 |
| C 127 | 15 | 2.4 | 677 | 1 | US-08-211-942-8 | Sequence 8, Appl1 | 200 | 15 | 2.4 | 2210 | 1 | US-07-710-361-2 | Sequence 2, Appl1 |
| C 128 | 15 | 2.4 | 732 | 1 | US-08-211-942-6 | Sequence 6, Appl1 | 201 | 15 | 2.4 | 2217 | 4 | US-09-107-532A-1442 | Sequence 1442, Ap |
| C 129 | 15 | 2.4 | 747 | 4 | US-09-328-352-2295 | Sequence 2295, Ap | 202 | 15 | 2.4 | 2220 | 4 | US-09-134-001C-749 | Sequence 749, Ap |
| C 130 | 15 | 2.4 | 765 | 2 | US-08-667-939A-12 | Sequence 12, Appl1 | 203 | 15 | 2.4 | 2249 | 2 | US-08-463-081B-34 | Sequence 34, Appl1 |
| C 131 | 15 | 2.4 | 765 | 2 | US-08-667-939A-13 | Sequence 13, Appl1 | 204 | 15 | 2.4 | 2249 | 2 | US-08-461-379A-34 | Sequence 34, Appl1 |
| C 132 | 15 | 2.4 | 765 | 2 | US-08-667-939A-14 | Sequence 14, Appl1 | 205 | 15 | 2.4 | 2249 | 2 | US-08-462-390B-34 | Sequence 34, Appl1 |
| C 133 | 15 | 2.4 | 765 | 2 | US-08-667-939A-15 | Sequence 15, Appl1 | 206 | 15 | 2.4 | 2249 | 3 | US-08-463-074B-34 | Sequence 34, Appl1 |
| C 134 | 15 | 2.4 | 765 | 2 | US-08-667-939A-16 | Sequence 16, Appl1 | 207 | 15 | 2.4 | 2249 | 3 | US-08-465-585C-34 | Sequence 34, Appl1 |
| C 135 | 15 | 2.4 | 765 | 4 | US-08-433-123-12 | Sequence 12, Appl1 | 208 | 15 | 2.4 | 2249 | 3 | US-08-652-446-34 | Sequence 34, Appl1 |
| C 136 | 15 | 2.4 | 765 | 4 | US-08-433-123-13 | Sequence 13, Appl1 | 209 | 15 | 2.4 | 2249 | 3 | US-09-802-117-5 | Sequence 5, Appl1 |
| C 137 | 15 | 2.4 | 765 | 4 | US-08-433-123-14 | Sequence 14, Appl1 | 210 | 15 | 2.4 | 2288 | 3 | US-09-135-232-1 | Sequence 1, Appl1 |
| C 138 | 15 | 2.4 | 765 | 4 | US-08-433-123-15 | Sequence 15, Appl1 | 211 | 15 | 2.4 | 2288 | 4 | US-09-026-001A-11 | Sequence 11, Appl1 |
| C 139 | 15 | 2.4 | 803 | 4 | US-09-634-238-70 | Sequence 70, Appl1 | 212 | 15 | 2.4 | 2288 | 4 | US-09-863-549-1 | Sequence 1, Appl1 |
| C 140 | 15 | 2.4 | 831 | 4 | US-09-328-475C-453 | Sequence 253, Ap | 213 | 15 | 2.4 | 2327 | 2 | US-08-835-170-3 | Sequence 3, Appl1 |
| C 141 | 15 | 2.4 | 870 | 4 | US-09-328-352-1901 | Sequence 1901, Ap | 214 | 15 | 2.4 | 2327 | 3 | US-09-359-257-3 | Sequence 3, Appl1 |
| C 142 | 15 | 2.4 | 870 | 4 | US-09-314-701-55 | Sequence 55, Appl1 | 215 | 15 | 2.4 | 2327 | 4 | US-09-371-674-3 | Sequence 3, Appl1 |
| C 143 | 15 | 2.4 | 891 | 4 | US-09-328-352-3786 | Sequence 3786, Ap | 216 | 15 | 2.4 | 2334 | 4 | US-08-062-632-4 | Sequence 4, Appl1 |
| C 144 | 15 | 2.4 | 933 | 4 | US-09-107-532A-1271 | Sequence 1271, Ap | 217 | 15 | 2.4 | 2347 | 5 | PCT-US96-03965-1 | Sequence 1, Appl1 |
| C 145 | 15 | 2.4 | 942 | 4 | US-09-382-906A-1 | Sequence 1, Appl1 | 218 | 15 | 2.4 | 2350 | 4 | US-08-012-269A-1 | Sequence 1, Appl1 |
| C 146 | 15 | 2.4 | 957 | 4 | US-09-328-352-2278 | Sequence 2278, Ap | 219 | 15 | 2.4 | 2383 | 3 | US-09-523-467-9 | Sequence 9, Appl1 |
| C 147 | 15 | 2.4 | 960 | 4 | US-09-671-317-23 | Sequence 23, Appl1 | 220 | 15 | 2.4 | 2400 | 1 | US-08-785-052-3 | Sequence 3, Appl1 |
| C 148 | 15 | 2.4 | 1001 | 4 | US-09-671-317-176 | Sequence 176, Ap | 221 | 15 | 2.4 | 2409 | 2 | US-09-320-095-9 | Sequence 9, Appl1 |
| C 149 | 15 | 2.4 | 1001 | 4 | US-09-671-317-176 | Sequence 176, Ap | 222 | 15 | 2.4 | 2409 | 3 | US-09-328-352-2551 | Sequence 2551, Ap |
| C 150 | 15 | 2.4 | 1026 | 4 | US-09-328-352-3052 | Sequence 3052, Ap | 223 | 15 | 2.4 | 2451 | 4 | US-09-328-352-70 | Sequence 70, Appl1 |
| C 151 | 15 | 2.4 | 1047 | 4 | US-09-107-532A-2496 | Sequence 2496, Ap | 224 | 15 | 2.4 | 2562 | 4 | US-09-620-312D-1034 | Sequence 1034, Ap |
| C 152 | 15 | 2.4 | 1110 | 4 | US-09-328-352-171 | Sequence 171, Ap | 225 | 15 | 2.4 | 2576 | 4 | US-09-068-740A-8 | Sequence 8, Appl1 |
| C 153 | 15 | 2.4 | 1131 | 4 | US-09-620-312D-203 | Sequence 203, Ap | 226 | 15 | 2.4 | 2663 | 3 | US-09-061-768A-1 | Sequence 1, Appl1 |
| C 154 | 15 | 2.4 | 1169 | 3 | US-08-903-325-4 | Sequence 4, Appl1 | 227 | 15 | 2.4 | 2685 | 3 | US-08-481-130-25 | Sequence 25, Appl1 |
| C 155 | 15 | 2.4 | 1182 | 4 | US-09-107-532A-743 | Sequence 743, Ap | 228 | 15 | 2.4 | 2775 | 1 | US-08-656-984A-25 | Sequence 25, Appl1 |
| C 156 | 15 | 2.4 | 1251 | 3 | US-09-330-611-1 | Sequence 1, Appl1 | 229 | 15 | 2.4 | 2775 | 1 | US-08-485-604-25 | Sequence 25, Appl1 |
| C 157 | 15 | 2.4 | 1251 | 3 | US-08-591-662-1 | Sequence 1, Appl1 | 230 | 15 | 2.4 | 2775 | 1 | US-08-487-595-25 | Sequence 25, Appl1 |
| C 158 | 15 | 2.4 | 1282 | 1 | US-08-211-942-16 | Sequence 16, Appl1 | 231 | 15 | 2.4 | 2910 | 2 | US-08-375-709-6 | Sequence 6, Appl1 |
| C 159 | 15 | 2.4 | 1299 | 4 | US-09-222-938A-39 | Sequence 39, Appl1 | 232 | 15 | 2.4 | 2910 | 1 | US-08-752-929-6 | Sequence 6, Appl1 |
| C 160 | 15 | 2.4 | 1339 | 3 | US-08-855-910-5 | Sequence 5, Appl1 | 233 | 15 | 2.4 | 2910 | 4 | US-09-231-899-81 | Sequence 81, Appl1 |
| C 161 | 15 | 2.4 | 1431 | 1 | US-07-865-662F-11 | Sequence 11, Appl1 | 234 | 15 | 2.4 | 2999 | 2 | US-09-014-969-8 | Sequence 8, Appl1 |
| C 162 | 15 | 2.4 | 1487 | 3 | US-08-374-219B-11 | Sequence 11, Appl1 | 235 | 15 | 2.4 | 3054 | 1 | US-08-434-730-15 | Sequence 15, Appl1 |
| C 163 | 15 | 2.4 | 1503 | 4 | US-09-328-352-4057 | Sequence 4057, Ap | 236 | 15 | 2.4 | 3073 | 4 | US-07-668-352C-31 | Sequence 31, Appl1 |
| C 164 | 15 | 2.4 | 1551 | 4 | US-09-623-972-19 | Sequence 19, Appl1 | 237 | 15 | 2.4 | 3073 | 2 | US-08-474-379C-31 | Sequence 31, Appl1 |
| C 165 | 15 | 2.4 | 1620 | 2 | US-08-874-186-37 | Sequence 37, Appl1 | 238 | 15 | 2.4 | 3073 | 3 | US-09-146-249A-31 | Sequence 31, Appl1 |
| C 166 | 15 | 2.4 | 1642 | 4 | US-09-737-698B-24 | Sequence 24, Appl1 | 239 | 15 | 2.4 | 3073 | 3 | US-08-206-188B-31 | Sequence 31, Appl1 |

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| 247 | 15 | 2.4 | 3073 | 5 | PCT-US91-02714-30 | Sequence 30, Appl | 320 | 15 | 2.4 | 7560 | 3 | US-09-103-478-4 | Sequence 4, Appl |
| 248 | 15 | 2.4 | 3266 | 4 | US-08-485-511A-3 | Sequence 3, Appl | 321 | 15 | 2.4 | 7560 | 4 | US-09-193-931C-4 | Sequence 4, Appl |
| 249 | 15 | 2.4 | 3412 | 3 | US-08-903-325-3 | Sequence 3, Appl | 322 | 15 | 2.4 | 7560 | 4 | US-09-026-221-1 | Sequence 4, Appl |
| 250 | 15 | 2.4 | 3505 | 1 | US-07-660-465-1 | Sequence 1, Appl | 323 | 15 | 2.4 | 8378 | 5 | PCT-US91-09055-1 | Sequence 1, Appl |
| 251 | 15 | 2.4 | 3632 | 1 | US-08-424-788-4 | Sequence 1, Appl | 324 | 15 | 2.4 | 9641 | 4 | US-09-625-972-22 | Sequence 2, Appl |
| 252 | 15 | 2.4 | 3632 | 1 | US-08-110-683-1 | Sequence 1, Appl | 325 | 15 | 2.4 | 10640 | 4 | US-09-417-4850-5 | Sequence 5, Appl |
| 253 | 15 | 2.4 | 3632 | 2 | US-08-683-743-1 | Sequence 1, Appl | 326 | 15 | 2.4 | 12597 | 4 | US-09-705-299-12 | Sequence 12, Appl |
| 254 | 15 | 2.4 | 3632 | 2 | US-08-477-166-1 | Sequence 1, Appl | 327 | 15 | 2.4 | 14796 | 3 | US-08-975-080-35 | Sequence 33, Appl |
| 255 | 15 | 2.4 | 3632 | 2 | US-08-472-097-1 | Sequence 1, Appl | 328 | 15 | 2.4 | 14796 | 3 | US-09-630-706-10 | Sequence 10, Appl |
| 256 | 15 | 2.4 | 3632 | 4 | US-09-439-672-1 | Sequence 1, Appl | 329 | 15 | 2.4 | 14796 | 4 | US-09-496-694A-3 | Sequence 3, Appl |
| 257 | 15 | 2.4 | 3632 | 4 | US-09-495-052-57 | Sequence 57, Appl | 330 | 15 | 2.4 | 15378 | 3 | US-08-785-420-1 | Sequence 1, Appl |
| 258 | 15 | 2.4 | 3632 | 5 | PCT-US93-11638-1 | Sequence 1, Appl | 331 | 15 | 2.4 | 20966 | 4 | US-08-961-527-54 | Sequence 54, Appl |
| 259 | 15 | 2.4 | 3735 | 4 | US-09-620-312D-52 | Sequence 52, Appl | 332 | 15 | 2.4 | 25464 | 4 | US-09-326-480A-96 | Sequence 4, Appl |
| 260 | 15 | 2.4 | 3780 | 4 | US-09-134-001C-920 | Sequence 920, App | 333 | 15 | 2.4 | 30310 | 4 | US-09-657-446A-96 | Sequence 96, Appl |
| 261 | 15 | 2.4 | 3883 | 4 | US-09-620-312D-792 | Sequence 792, App | 334 | 15 | 2.4 | 34466 | 4 | US-09-103-330-35 | Sequence 35, Appl |
| 262 | 15 | 2.4 | 3934 | 3 | US-09-226-568-18 | Sequence 18, Appl | 335 | 15 | 2.4 | 36651 | 4 | US-09-738-894A-3 | Sequence 3, Appl |
| 263 | 15 | 2.4 | 3946 | 1 | US-08-077-848A-1 | Sequence 1, Appl | 336 | 15 | 2.4 | 36651 | 4 | US-09-964-669-3 | Sequence 3, Appl |
| 264 | 15 | 2.4 | 3946 | 3 | US-09-211-640-1 | Sequence 1, Appl | 337 | 15 | 2.4 | 37895 | 1 | US-08-375-709-1 | Sequence 1, Appl |
| 265 | 15 | 2.4 | 3946 | 3 | US-09-378-536-1 | Sequence 1, Appl | 338 | 15 | 2.4 | 37895 | 1 | US-08-752-929-1 | Sequence 1, Appl |
| 266 | 15 | 2.4 | 3946 | 4 | US-09-687-260-1 | Sequence 1, Appl | 339 | 15 | 2.4 | 37895 | 3 | US-09-090-793-1 | Sequence 1, Appl |
| 267 | 15 | 2.4 | 3946 | 5 | PCT-US94-03547-1 | Sequence 1, Appl | 340 | 15 | 2.4 | 37895 | 4 | US-09-231-899-1 | Sequence 1, Appl |
| 268 | 15 | 2.4 | 3986 | 2 | US-08-627-254C-27 | Sequence 27, Appl | 341 | 15 | 2.4 | 45175 | 4 | US-09-453-702B-116 | Sequence 116, App |
| 269 | 15 | 2.4 | 4049 | 1 | US-08-162-809-17 | Sequence 17, Appl | 342 | 15 | 2.4 | 49785 | 4 | US-09-453-702B-60 | Sequence 60, Appl |
| 270 | 15 | 2.4 | 4060 | 1 | US-08-164-292B-1 | Sequence 1, Appl | 343 | 15 | 2.4 | 62804 | 4 | US-09-800-960-3 | Sequence 3, Appl |
| 271 | 15 | 2.4 | 4060 | 1 | US-08-164-292B-3 | Sequence 3, Appl | 344 | 15 | 2.4 | 63588 | 4 | US-09-873-404-3 | Sequence 3, Appl |
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| 275 | 15 | 2.4 | 4060 | 3 | US-08-845-623-3 | Sequence 3, Appl | 348 | 15 | 2.4 | 116884 | 4 | US-09-661-596A-76 | Sequence 76, Appl |
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| 279 | 15 | 2.4 | 4060 | 3 | US-08-815-927-3 | Sequence 3, Appl | 352 | 15 | 2.4 | 580073 | 4 | US-08-545-528D-1 | Sequence 1, Appl |
| 280 | 15 | 2.4 | 4060 | 3 | US-08-815-927-5 | Sequence 5, Appl | 353 | 14 | 2.3 | 20 | 2 | US-08-837-201C-31 | Sequence 31, Appl |
| 281 | 15 | 2.4 | 4060 | 3 | US-08-815-927-7 | Sequence 7, Appl | 354 | 14 | 2.3 | 20 | 4 | US-09-364-416-31 | Sequence 31, Appl |
| 282 | 15 | 2.4 | 4060 | 4 | US-09-103-330-1 | Sequence 1, Appl | 355 | 14 | 2.3 | 20 | 4 | US-09-198-452A-6558 | Sequence 6558, Ap |
| 283 | 15 | 2.4 | 4060 | 4 | US-09-103-330-3 | Sequence 3, Appl | 356 | 14 | 2.3 | 21 | 1 | US-08-211-430-26 | Sequence 26, Appl |
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| 287 | 15 | 2.4 | 4060 | 4 | US-09-435-242-3 | Sequence 3, Appl | 360 | 14 | 2.3 | 56 | 1 | US-08-081-539-47 | Sequence 47, Appl |
| 288 | 15 | 2.4 | 4060 | 4 | US-09-435-242-5 | Sequence 5, Appl | 361 | 14 | 2.3 | 56 | 1 | US-08-466-647-47 | Sequence 47, Appl |
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| 290 | 15 | 2.4 | 4060 | 2 | US-08-568-459A-1 | Sequence 1, Appl | 363 | 14 | 2.3 | 58 | 1 | US-08-466-647-46 | Sequence 46, Appl |
| 291 | 15 | 2.4 | 4084 | 4 | US-08-487-826B-1 | Sequence 1, Appl | 364 | 14 | 2.3 | 59 | 3 | US-07-602-848E-11 | Sequence 11, Appl |
| 292 | 15 | 2.4 | 4084 | 4 | US-09-210-288-1 | Sequence 1, Appl | 365 | 14 | 2.3 | 64 | 3 | US-08-516-859A-95 | Sequence 95, Appl |
| 293 | 15 | 2.4 | 4084 | 6 | 5198347-5 | Patent No. 5198347 | 366 | 14 | 2.3 | 64 | 4 | US-09-586-472-95 | Sequence 95, Appl |
| 294 | 15 | 2.4 | 4097 | 1 | US-08-162-809-11 | Sequence 11, Appl | 367 | 14 | 2.3 | 91 | 4 | US-09-528-706-95 | Sequence 95, Appl |
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| 296 | 15 | 2.4 | 4121 | 4 | US-09-604-978-4 | Sequence 4, Appl | 369 | 14 | 2.3 | 165 | 3 | US-08-816-346-37 | Sequence 37, Appl |
| 297 | 15 | 2.4 | 4334 | 2 | US-08-670-707A-38 | Sequence 38, Appl | 370 | 14 | 2.3 | 165 | 3 | US-09-335-411-37 | Sequence 37, Appl |
| 298 | 15 | 2.4 | 4334 | 3 | US-09-037-601-38 | Sequence 38, Appl | 371 | 14 | 2.3 | 194 | 4 | US-09-702-705-1450 | Sequence 1450, Ap |
| 299 | 15 | 2.4 | 4334 | 3 | US-09-315-179-8 | Sequence 38, Appl | 372 | 14 | 2.3 | 194 | 4 | US-09-736-457-1450 | Sequence 1450, Ap |
| 300 | 15 | 2.4 | 4334 | 3 | US-09-187-049-1 | Sequence 1, Appl | 373 | 14 | 2.3 | 205 | 1 | US-07-687-466B-3 | Sequence 3, Appl |
| 301 | 15 | 2.4 | 4404 | 4 | US-09-523-656-37 | Sequence 37, Appl | 374 | 14 | 2.3 | 235 | 4 | US-09-107-532A-1774 | Sequence 1774, Ap |
| 302 | 15 | 2.4 | 4832 | 4 | US-09-457-037B-2 | Sequence 2, Appl | 375 | 14 | 2.3 | 235 | 4 | US-09-134-001C-84 | Sequence 84, Appl |
| 303 | 15 | 2.4 | 4832 | 4 | US-09-733-151-2 | Sequence 2, Appl | 376 | 14 | 2.3 | 241 | 4 | US-09-016-434-7-146 | Sequence 746, App |
| 304 | 15 | 2.4 | 4832 | 4 | US-08-110-158-5 | Sequence 5, Appl | 377 | 14 | 2.3 | 258 | 4 | US-09-134-001C-1148 | Sequence 1148, Ap |
| 305 | 15 | 2.4 | 4946 | 3 | US-08-817-188-1 | Sequence 1, Appl | 378 | 14 | 2.3 | 265 | 4 | US-09-280-116-33 | Sequence 33, Appl |
| 306 | 15 | 2.4 | 4946 | 4 | US-09-457-037B-1 | Sequence 1, Appl | 379 | 14 | 2.3 | 273 | 4 | US-09-134-001C-2061 | Sequence 2061, Ap |
| 307 | 15 | 2.4 | 4946 | 4 | US-09-733-151-1 | Sequence 1, Appl | 380 | 14 | 2.3 | 275 | 4 | US-09-702-705-1243 | Sequence 1243, Ap |
| 308 | 15 | 2.4 | 5864 | 3 | US-08-894-440-4 | Sequence 4, Appl | 381 | 14 | 2.3 | 275 | 4 | US-09-736-457-1243 | Sequence 1243, Ap |
| 309 | 15 | 2.4 | 5864 | 3 | US-09-458-093-4 | Sequence 4, Appl | 382 | 14 | 2.3 | 280 | 4 | US-09-313-294A-831 | Sequence 831, App |
| 310 | 15 | 2.4 | 5865 | 4 | US-09-430-487A-1 | Sequence 1, Appl | 383 | 14 | 2.3 | 292 | 3 | US-09-037-690B-15 | Sequence 15, Appl |
| 311 | 15 | 2.4 | 6030 | 1 | US-08-441-139-8 | Sequence 8, Appl | 384 | 14 | 2.3 | 294 | 4 | US-09-134-001C-2032 | Sequence 2032, Ap |
| 312 | 15 | 2.4 | 6230 | 1 | US-09-620-312D-459 | Sequence 459, App | 385 | 14 | 2.3 | 294 | 4 | US-09-313-294A-6046 | Sequence 6046, Ap |
| 313 | 15 | 2.4 | 6304 | 4 | US-09-620-312D-461 | Sequence 461, App | 386 | 14 | 2.3 | 297 | 4 | US-09-313-294A-7286 | Sequence 7286, Ap |
| 314 | 15 | 2.4 | 6382 | 4 | US-09-620-312D-460 | Sequence 36, App | 387 | 14 | 2.3 | 300 | 4 | US-09-313-294A-6323 | Sequence 6323, Ap |
| 315 | 15 | 2.4 | 6402 | 2 | US-08-670-707A-36 | Sequence 36, Appl | 388 | 14 | 2.3 | 300 | 4 | US-09-205-258-143 | Sequence 143, App |
| 316 | 15 | 2.4 | 6402 | 3 | US-09-037-601-36 | Sequence 36, Appl | 389 | 14 | 2.3 | 307 | 4 | US-09-313-294A-6024 | Sequence 6024, Ap |
| 317 | 15 | 2.4 | 6402 | 3 | US-09-315-179-36 | Sequence 36, Appl | 390 | 14 | 2.3 | 315 | 1 | US-08-081-539-89 | Sequence 89, Appl |
| 318 | 15 | 2.4 | 6402 | 4 | US-09-523-656-29 | Sequence 29, Appl | 391 | 14 | 2.3 | 315 | 1 | US-08-466-647-89 | Sequence 89, Appl |
| 319 | 15 | 2.4 | 6474 | 4 | US-08-961-527-155 | Sequence 155, App | 392 | 14 | 2.3 | 332 | 3 | US-08-943-731-106 | Sequence 106, Appl |

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| 393 | 14 | 2.3 | 357 | 4 | US-09-134-001C-802 | Sequence 802, App | 466 | 14 | 2.3 | 526 | 1 | US-08-700-575-1 | Sequence 1, Appl |
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| 395 | 14 | 2.3 | 361 | 3 | US-08-905-223-142 | Sequence 142, App | 468 | 14 | 2.3 | 546 | 4 | US-09-328-352-180 | Sequence 180, App |
| 396 | 14 | 2.3 | 369 | 3 | US-08-991-789A-190 | Sequence 190, App | C 469 | 14 | 2.3 | 549 | 4 | US-09-328-352-1559 | Sequence 1559, App |
| 397 | 14 | 2.3 | 369 | 4 | US-09-062-451-190 | Sequence 190, App | 470 | 14 | 2.3 | 552 | 4 | US-09-702-705-712 | Sequence 712, App |
| 398 | 14 | 2.3 | 369 | 4 | US-09-598-326-190 | Sequence 190, App | 471 | 14 | 2.3 | 552 | 4 | US-09-736-457-712 | Sequence 712, App |
| 399 | 14 | 2.3 | 369 | 4 | US-09-289-198-190 | Sequence 190, App | 472 | 14 | 2.3 | 573 | 3 | US-09-328-111-221 | Sequence 221, App |
| C 400 | 14 | 2.3 | 372 | 4 | US-09-702-705-226 | Sequence 226, App | 473 | 14 | 2.3 | 588 | 3 | US-09-328-111-221 | Sequence 221, App |
| C 401 | 14 | 2.3 | 372 | 4 | US-09-736-457-1906 | Sequence 226, App | C 474 | 14 | 2.3 | 590 | 1 | US-08-463-115-15 | Sequence 321, App |
| C 402 | 14 | 2.3 | 372 | 4 | US-09-328-352-1296 | Sequence 1906, App | C 475 | 14 | 2.3 | 590 | 1 | US-08-463-115-15 | Sequence 321, App |
| C 403 | 14 | 2.3 | 372 | 4 | US-09-328-352-2837 | Sequence 2837, App | C 476 | 14 | 2.3 | 592 | 4 | US-08-585-593A-27 | Sequence 27, Appl |
| C 404 | 14 | 2.3 | 375 | 4 | US-09-328-352-3725 | Sequence 3725, App | C 477 | 14 | 2.3 | 597 | 4 | US-09-328-352-825 | Sequence 825, App |
| C 405 | 14 | 2.3 | 380 | 4 | US-09-288-143-53 | Sequence 53, App | C 478 | 14 | 2.3 | 610 | 4 | US-09-221-017B-1069 | Sequence 1069, App |
| C 406 | 14 | 2.3 | 399 | 3 | US-09-242-216-1 | Sequence 1, Appl | C 479 | 14 | 2.3 | 613 | 4 | US-09-149-476-15 | Sequence 15, Appl |
| C 407 | 14 | 2.3 | 399 | 4 | US-09-134-001C-1761 | Sequence 1761, App | C 480 | 14 | 2.3 | 618 | 1 | US-08-155-171B-5 | Sequence 15, Appl |
| C 408 | 14 | 2.3 | 414 | 4 | US-09-071-035-53 | Sequence 53, Appl | C 481 | 14 | 2.3 | 618 | 2 | US-08-435-998-5 | Sequence 5, Appl |
| C 409 | 14 | 2.3 | 415 | 2 | US-08-481-658B-28 | Sequence 28, Appl | C 482 | 14 | 2.3 | 630 | 4 | US-09-134-001C-1143 | Sequence 1143, App |
| C 410 | 14 | 2.3 | 415 | 2 | US-08-477-504A-28 | Sequence 28, Appl | C 483 | 14 | 2.3 | 631 | 4 | US-09-059-625-41 | Sequence 41, Appl |
| C 411 | 14 | 2.3 | 415 | 2 | US-08-486-756A-28 | Sequence 28, Appl | C 484 | 14 | 2.3 | 639 | 4 | US-09-134-001C-2133 | Sequence 2133, App |
| C 412 | 14 | 2.3 | 415 | 2 | US-08-485-862B-28 | Sequence 28, Appl | C 485 | 14 | 2.3 | 642 | 4 | US-09-107-532A-1906 | Sequence 1906, App |
| C 413 | 14 | 2.3 | 415 | 3 | US-08-487-077A-28 | Sequence 28, Appl | C 486 | 14 | 2.3 | 645 | 4 | US-09-134-001C-1986 | Sequence 1986, App |
| C 414 | 14 | 2.3 | 415 | 3 | US-08-485-863A-28 | Sequence 28, Appl | C 487 | 14 | 2.3 | 648 | 1 | US-07-872-678A-3 | Sequence 3, Appl |
| C 415 | 14 | 2.3 | 415 | 3 | US-08-485-049D-28 | Sequence 28, Appl | C 488 | 14 | 2.3 | 653 | 3 | US-08-998-416-46 | Sequence 46, Appl |
| C 416 | 14 | 2.3 | 425 | 4 | US-09-000-266-25 | Sequence 25, Appl | C 489 | 14 | 2.3 | 657 | 3 | US-09-037-990B-2 | Sequence 2, Appl |
| C 417 | 14 | 2.3 | 425 | 4 | US-09-000-266-27 | Sequence 27, Appl | C 490 | 14 | 2.3 | 660 | 4 | US-09-702-705-176 | Sequence 176, App |
| C 418 | 14 | 2.3 | 425 | 4 | US-09-628-099-25 | Sequence 25, Appl | C 491 | 14 | 2.3 | 660 | 4 | US-09-736-457-176 | Sequence 176, App |
| C 419 | 14 | 2.3 | 425 | 4 | US-09-628-099-27 | Sequence 25, Appl | C 492 | 14 | 2.3 | 666 | 4 | US-09-435-019-11 | Sequence 11, Appl |
| C 420 | 14 | 2.3 | 425 | 4 | US-10-056-360-25 | Sequence 25, Appl | C 493 | 14 | 2.3 | 666 | 4 | US-09-435-019-12 | Sequence 12, Appl |
| C 421 | 14 | 2.3 | 425 | 4 | US-10-056-360-27 | Sequence 27, Appl | C 494 | 14 | 2.3 | 670 | 3 | US-09-040-984-7 | Sequence 7, Appl |
| C 422 | 14 | 2.3 | 425 | 4 | US-10-056-359-25 | Sequence 25, Appl | C 495 | 14 | 2.3 | 670 | 4 | US-09-123-912-7 | Sequence 7, Appl |
| C 423 | 14 | 2.3 | 433 | 2 | US-08-056-359-27 | Sequence 27, Appl | C 496 | 14 | 2.3 | 670 | 4 | US-09-643-597-7 | Sequence 7, Appl |
| C 424 | 14 | 2.3 | 433 | 2 | US-08-592-541-34 | Sequence 34, Appl | C 497 | 14 | 2.3 | 670 | 4 | US-09-480-884A-7 | Sequence 7, Appl |
| C 425 | 14 | 2.3 | 433 | 3 | US-09-124-698-34 | Sequence 34, Appl | C 498 | 14 | 2.3 | 670 | 4 | US-09-542-615A-7 | Sequence 7, Appl |
| C 426 | 14 | 2.3 | 433 | 3 | US-09-127-480-34 | Sequence 34, Appl | C 499 | 14 | 2.3 | 670 | 4 | US-09-606-41B-7 | Sequence 7, Appl |
| C 427 | 14 | 2.3 | 433 | 3 | US-08-496-841C-34 | Sequence 34, Appl | C 500 | 14 | 2.3 | 678 | 4 | US-09-205-258-187 | Sequence 187, App |
| C 428 | 14 | 2.3 | 433 | 3 | US-09-124-523-34 | Sequence 34, Appl | C 501 | 14 | 2.3 | 681 | 4 | US-09-410-464-3 | Sequence 3, Appl |
| C 429 | 14 | 2.3 | 433 | 4 | US-09-636-796A-34 | Sequence 34, Appl | C 502 | 14 | 2.3 | 686 | 1 | US-08-591-498-15 | Sequence 15, Appl |
| C 430 | 14 | 2.3 | 433 | 4 | US-08-431-048P-34 | Sequence 34, Appl | C 503 | 14 | 2.3 | 688 | 1 | US-08-463-115-40 | Sequence 44, Appl |
| C 431 | 14 | 2.3 | 435 | 4 | US-09-007-119-3 | Sequence 3, Appl | C 504 | 14 | 2.3 | 688 | 1 | US-08-463-388-44 | Sequence 44, Appl |
| C 432 | 14 | 2.3 | 435 | 4 | US-08-787-739-28 | Sequence 28, Appl | C 505 | 14 | 2.3 | 716 | 3 | US-08-998-416-795 | Sequence 795, App |
| C 433 | 14 | 2.3 | 445 | 3 | US-09-178-115-28 | Sequence 28, Appl | C 506 | 14 | 2.3 | 717 | 4 | US-09-328-352-887 | Sequence 887, App |
| C 434 | 14 | 2.3 | 445 | 3 | US-09-177-776-28 | Sequence 28, Appl | C 507 | 14 | 2.3 | 719 | 3 | US-08-983-409-6 | Sequence 6, Appl |
| C 435 | 14 | 2.3 | 446 | 3 | US-09-097-541-1 | Sequence 1, Appl | C 508 | 14 | 2.3 | 721 | 4 | US-09-663-600A-65 | Sequence 65, Appl |
| C 436 | 14 | 2.3 | 446 | 4 | US-09-333-214-1 | Sequence 1, Appl | C 509 | 14 | 2.3 | 726 | 4 | US-09-134-001C-2091 | Sequence 2091, App |
| C 437 | 14 | 2.3 | 447 | 4 | US-09-134-001C-2777 | Sequence 2777, App | C 510 | 14 | 2.3 | 729 | 4 | US-09-059-625-43 | Sequence 33, Appl |
| C 438 | 14 | 2.3 | 453 | 4 | US-09-134-001C-2664 | Sequence 2664, App | C 511 | 14 | 2.3 | 729 | 4 | US-09-059-625-44 | Sequence 44, Appl |
| C 439 | 14 | 2.3 | 453 | 4 | US-09-134-001C-2664 | Sequence 2664, App | C 512 | 14 | 2.3 | 735 | 4 | US-09-107-532A-235 | Sequence 235, App |
| C 440 | 14 | 2.3 | 461 | 4 | US-09-536-051C-2664 | Sequence 18, Appl | C 513 | 14 | 2.3 | 750 | 4 | US-09-252-991A-10876 | Sequence 10876, A |
| C 441 | 14 | 2.3 | 467 | 3 | US-09-328-111-329 | Sequence 329, App | C 514 | 14 | 2.3 | 765 | 4 | US-09-328-352-1067 | Sequence 3067, App |
| C 442 | 14 | 2.3 | 468 | 4 | US-09-107-532A-1610 | Sequence 1610, App | C 515 | 14 | 2.3 | 783 | 4 | US-09-134-001C-1622 | Sequence 1622, App |
| C 443 | 14 | 2.3 | 475 | 2 | US-08-623-906A-4 | Sequence 4, Appl | C 516 | 14 | 2.3 | 783 | 5 | PCT-US92-00282-22 | Sequence 22, Appl |
| C 444 | 14 | 2.3 | 483 | 4 | US-09-306-564-4 | Sequence 4, Appl | C 517 | 14 | 2.3 | 798 | 4 | US-09-463-451-25 | Sequence 25, Appl |
| C 445 | 14 | 2.3 | 486 | 1 | US-08-048-164A-1 | Sequence 1, Appl | C 518 | 14 | 2.3 | 798 | 4 | US-09-463-451-25 | Sequence 25, Appl |
| C 446 | 14 | 2.3 | 486 | 1 | US-08-048-164A-3 | Sequence 3, Appl | C 519 | 14 | 2.3 | 799 | 4 | US-09-166-350-11 | Sequence 11, Appl |
| C 447 | 14 | 2.3 | 486 | 1 | US-08-460-462-1 | Sequence 1, Appl | C 520 | 14 | 2.3 | 801 | 4 | US-09-134-001C-2084 | Sequence 2084, App |
| C 448 | 14 | 2.3 | 486 | 1 | US-08-460-462-1 | Sequence 1, Appl | C 521 | 14 | 2.3 | 807 | 4 | US-09-328-352-2003 | Sequence 2003, App |
| C 449 | 14 | 2.3 | 486 | 1 | US-08-460-462-1 | Sequence 1, Appl | C 522 | 14 | 2.3 | 811 | 3 | US-08-961-083-197 | Sequence 197, App |
| C 450 | 14 | 2.3 | 486 | 1 | US-08-460-462-1 | Sequence 1, Appl | C 523 | 14 | 2.3 | 811 | 4 | US-09-536-784-197 | Sequence 197, App |
| C 451 | 14 | 2.3 | 486 | 1 | US-08-460-462-1 | Sequence 1, Appl | C 524 | 14 | 2.3 | 816 | 4 | US-09-134-001C-2462 | Sequence 2462, App |
| C 452 | 14 | 2.3 | 486 | 1 | US-08-460-462-1 | Sequence 1, Appl | C 525 | 14 | 2.3 | 825 | 3 | US-09-250-677-1 | Sequence 1, Appl |
| C 453 | 14 | 2.3 | 486 | 2 | US-08-460-462-1 | Sequence 1, Appl | C 526 | 14 | 2.3 | 840 | 4 | US-09-328-352-1018 | Sequence 3018, App |
| C 454 | 14 | 2.3 | 486 | 2 | US-08-460-462-1 | Sequence 1, Appl | C 527 | 14 | 2.3 | 840 | 4 | US-09-328-352-3358 | Sequence 3358, App |
| C 455 | 14 | 2.3 | 486 | 2 | US-08-460-462-1 | Sequence 1, Appl | C 528 | 14 | 2.3 | 849 | 4 | US-09-107-532A-3358 | Sequence 801, App |
| C 456 | 14 | 2.3 | 486 | 2 | US-08-460-462-1 | Sequence 1, Appl | C 529 | 14 | 2.3 | 852 | 4 | US-09-134-001C-801 | Sequence 801, App |
| C 457 | 14 | 2.3 | 486 | 2 | US-08-330-394A-1 | Sequence 3, Appl | C 530 | 14 | 2.3 | 864 | 4 | US-09-107-532A-1107 | Sequence 1107, App |
| C 458 | 14 | 2.3 | 488 | 2 | US-09-280-116-90 | Sequence 90, Appl | C 531 | 14 | 2.3 | 866 | 3 | US-09-122-400B-4 | Sequence 4, Appl |
| C 459 | 14 | 2.3 | 499 | 3 | US-09-284-782-21 | Sequence 21, Appl | C 532 | 14 | 2.3 | 867 | 4 | US-09-134-001C-1168 | Sequence 1168, App |
| C 460 | 14 | 2.3 | 499 | 3 | US-09-006-632-5 | Sequence 5, Appl | C 533 | 14 | 2.3 | 870 | 4 | US-09-328-352-1901 | Sequence 1901, App |
| C 461 | 14 | 2.3 | 499 | 4 | US-09-006-632-5 | Sequence 5, Appl | C 534 | 14 | 2.3 | 888 | 4 | US-09-134-001C-752 | Sequence 752, App |
| C 462 | 14 | 2.3 | 499 | 4 | US-09-325-274-5 | Sequence 4, Appl | C 535 | 14 | 2.3 | 891 | 4 | US-09-328-352-1976 | Sequence 1976, App |
| C 463 | 14 | 2.3 | 504 | 1 | US-08-460-733-4 | Sequence 4, Appl | C 536 | 14 | 2.3 | 913 | 1 | US-08-217-327-3 | Sequence 3, Appl |
| C 464 | 14 | 2.3 | 508 | 4 | US-08-858-207A-227 | Sequence 227, App | C 537 | 14 | 2.3 | 913 | 1 | US-07-885-970A-3 | Sequence 3, Appl |
| C 465 | 14 | 2.3 | 516 | 4 | US-09-601-198-79 | Sequence 79, Appl | C 538 | 14 | 2.3 | 913 | 1 | US-08-298-687A-3 | Sequence 3, Appl |

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| 539 | 14 | 2.3 | 913 | 1 | US-08-530-797-2 | Sequence 2, Appli | C 612 | 14 | 2.3 | 1218 | 4 | US-09-252-991A-14561 | Sequence 14561, A |
| 540 | 14 | 2.3 | 913 | 1 | US-08-298-829-3 | Sequence 3, Appli | 613 | 14 | 2.3 | 1227 | 4 | US-09-134-001C-1293 | Sequence 1293, Ap |
| 541 | 14 | 2.3 | 913 | 2 | US-08-787-335-2 | Sequence 2, Appli | 614 | 14 | 2.3 | 1237 | 4 | US-09-134-001C-2376 | Sequence 2376, Ap |
| 542 | 14 | 2.3 | 924 | 4 | US-09-071-035-137 | Sequence 137, App | C 615 | 14 | 2.3 | 1242 | 4 | US-08-705-477E-95 | Sequence 95, Appl |
| 543 | 14 | 2.3 | 924 | 4 | US-09-252-991A-969 | Sequence 969, App | 616 | 14 | 2.3 | 1245 | 4 | US-09-134-001C-520 | Sequence 520, App |
| 544 | 14 | 2.3 | 927 | 4 | US-09-107-532A-271 | Sequence 271, App | C 617 | 14 | 2.3 | 1246 | 3 | US-09-236-080-1 | Sequence 1, Appli |
| 545 | 14 | 2.3 | 930 | 4 | US-09-328-352-3511 | Sequence 3511, Ap | 618 | 14 | 2.3 | 1247 | 3 | US-09-178-115-110 | Sequence 110, App |
| 546 | 14 | 2.3 | 933 | 4 | US-09-107-532A-558 | Sequence 558, App | 619 | 14 | 2.3 | 1247 | 3 | US-09-177-776-110 | Sequence 110, App |
| 547 | 14 | 2.3 | 939 | 1 | US-08-094-138A-26 | Sequence 26, Appl | C 620 | 14 | 2.3 | 1257 | 1 | US-08-161-286-3 | Sequence 3, Appli |
| 548 | 14 | 2.3 | 939 | 1 | US-08-455-674-26 | Sequence 26, Appl | 621 | 14 | 2.3 | 1260 | 1 | US-08-599-252-80 | Sequence 80, Appl |
| 549 | 14 | 2.3 | 939 | 1 | US-08-455-992-26 | Sequence 26, Appl | C 622 | 14 | 2.3 | 1260 | 1 | US-08-436-074-53 | Sequence 53, Appl |
| 550 | 14 | 2.3 | 939 | 1 | US-08-455-972-26 | Sequence 26, Appl | C 623 | 14 | 2.3 | 1260 | 1 | US-09-101-068-3 | Sequence 3, Appli |
| 551 | 14 | 2.3 | 939 | 1 | US-09-252-991A-925 | Sequence 925, App | 624 | 14 | 2.3 | 1260 | 5 | PCT-US96-06352-80 | Sequence 80, Appl |
| 552 | 14 | 2.3 | 939 | 5 | PCT-US92-00652-26 | Sequence 26, Appl | 625 | 14 | 2.3 | 1260 | 5 | PCT-US96-06583-80 | Sequence 80, Appl |
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| 556 | 14 | 2.3 | 948 | 4 | US-09-134-001C-2609 | Sequence 2609, Ap | 629 | 14 | 2.3 | 1282 | 4 | US-09-536-784-171 | Sequence 171, App |
| 557 | 14 | 2.3 | 949 | 4 | US-09-221-017B-615 | Sequence 615, App | C 630 | 14 | 2.3 | 1315 | 2 | US-08-087-797-1 | Sequence 1, Appli |
| 558 | 14 | 2.3 | 960 | 4 | US-09-107-532A-736 | Sequence 736, App | 631 | 14 | 2.3 | 1316 | 2 | US-08-684-687-3 | Sequence 3, Appli |
| 559 | 14 | 2.3 | 978 | 4 | US-09-328-352-3711 | Sequence 3711, Ap | 632 | 14 | 2.3 | 1316 | 4 | US-09-851-520-3 | Sequence 3, Appli |
| 560 | 14 | 2.3 | 996 | 4 | US-09-328-352-2703 | Sequence 2703, Ap | 633 | 14 | 2.3 | 1322 | 4 | US-09-634-238-178 | Sequence 178, App |
| 561 | 14 | 2.3 | 1000 | 2 | US-08-657-641-5 | Sequence 5, Appli | 634 | 14 | 2.3 | 1332 | 4 | US-09-107-532A-2409 | Sequence 2409, Ap |
| 562 | 14 | 2.3 | 1000 | 4 | US-09-671-317-343 | Sequence 343, App | C 635 | 14 | 2.3 | 1338 | 4 | US-09-252-991A-12084 | Sequence 12084, A |
| 563 | 14 | 2.3 | 1000 | 5 | PCT-US94-07233-5 | Sequence 5, Appli | C 636 | 14 | 2.3 | 1344 | 4 | US-09-388-349-6 | Sequence 6, Appli |
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| 565 | 14 | 2.3 | 1001 | 4 | US-09-641-638-92 | Sequence 92, Appl | C 638 | 14 | 2.3 | 1353 | 4 | US-09-134-001C-1974 | Sequence 1974, Ap |
| 566 | 14 | 2.3 | 1001 | 4 | US-09-641-638-93 | Sequence 93, Appl | 639 | 14 | 2.3 | 1364 | 1 | US-08-265-087-3 | Sequence 3, Appli |
| 567 | 14 | 2.3 | 1001 | 4 | US-09-641-638-94 | Sequence 94, Appl | 640 | 14 | 2.3 | 1364 | 1 | US-08-621-493-3 | Sequence 3, Appli |
| 568 | 14 | 2.3 | 1001 | 4 | US-09-641-638-94 | Sequence 94, Appl | 641 | 14 | 2.3 | 1364 | 2 | US-08-965-688-3 | Sequence 3, Appli |
| 569 | 14 | 2.3 | 1001 | 4 | US-09-641-638-187 | Sequence 187, App | 642 | 14 | 2.3 | 1364 | 3 | US-09-260-173-3 | Sequence 3, Appli |
| 570 | 14 | 2.3 | 1001 | 4 | US-09-641-638-304 | Sequence 304, App | 643 | 14 | 2.3 | 1368 | 4 | US-09-227-357-88 | Sequence 98, Appli |
| 571 | 14 | 2.3 | 1001 | 4 | US-09-641-638-367 | Sequence 367, App | C 644 | 14 | 2.3 | 1373 | 4 | US-09-996-243-7 | Sequence 7, Appli |
| 572 | 14 | 2.3 | 1001 | 4 | US-09-641-638-463 | Sequence 463, App | 645 | 14 | 2.3 | 1389 | 4 | US-09-328-352-1371 | Sequence 1371, Ap |
| 573 | 14 | 2.3 | 1001 | 4 | US-09-671-317-255 | Sequence 255, App | 646 | 14 | 2.3 | 1395 | 4 | US-09-924-703-5 | Sequence 5, Appli |
| 574 | 14 | 2.3 | 1001 | 4 | US-09-671-317-427 | Sequence 427, App | 647 | 14 | 2.3 | 1397 | 5 | PCT-US93-02024-1 | Sequence 1, Appli |
| 575 | 14 | 2.3 | 1005 | 4 | US-09-328-352-2366 | Sequence 2366, Ap | 648 | 14 | 2.3 | 1397 | 5 | PCT-US93-02024-1 | Sequence 1, Appli |
| 576 | 14 | 2.3 | 1006 | 3 | US-08-924-747-15 | Sequence 15, Appl | 649 | 14 | 2.3 | 1399 | 4 | US-08-335-469-1 | Sequence 1, Appli |
| 577 | 14 | 2.3 | 1006 | 3 | US-09-247-373B-15 | Sequence 15, Appl | 650 | 14 | 2.3 | 1399 | 4 | US-09-065-040-9 | Sequence 9, Appli |
| 578 | 14 | 2.3 | 1006 | 3 | US-09-247-373B-15 | Sequence 15, Appl | 651 | 14 | 2.3 | 1413 | 1 | US-08-104-445-1 | Sequence 1, Appli |
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| 580 | 14 | 2.3 | 1023 | 4 | US-09-134-001C-872 | Sequence 872, App | 653 | 14 | 2.3 | 1441 | 4 | US-09-302-495-8 | Sequence 8, Appli |
| 581 | 14 | 2.3 | 1033 | 4 | US-08-936-165A-7 | Sequence 7, Appli | 654 | 14 | 2.3 | 1441 | 4 | US-10-079-616-8 | Sequence 8, Appli |
| 582 | 14 | 2.3 | 1034 | 4 | US-09-702-705-1654 | Sequence 1654, Ap | 655 | 14 | 2.3 | 1451 | 4 | US-09-310-463-37 | Sequence 37, Appli |
| 583 | 14 | 2.3 | 1034 | 4 | US-09-736-457-1654 | Sequence 1654, Ap | 656 | 14 | 2.3 | 1458 | 4 | US-09-482-373-14 | Sequence 14, Appl |
| 584 | 14 | 2.3 | 1038 | 4 | US-09-252-991A-926 | Sequence 7926, Ap | 657 | 14 | 2.3 | 1470 | 4 | US-09-016-434-1203 | Sequence 1203, Ap |
| 585 | 14 | 2.3 | 1047 | 3 | US-09-137-885-3 | Sequence 3, Appli | 658 | 14 | 2.3 | 1472 | 4 | US-09-540-424-3 | Sequence 3, Appli |
| 586 | 14 | 2.3 | 1047 | 4 | US-09-723-548C-3 | Sequence 3, Appli | 659 | 14 | 2.3 | 1472 | 4 | US-09-564-595D-52 | Sequence 52, Appl |
| 587 | 14 | 2.3 | 1062 | 4 | US-09-134-001C-1488 | Sequence 1488, Ap | C 660 | 14 | 2.3 | 1482 | 4 | US-09-134-001C-1551 | Sequence 1551, Ap |
| 588 | 14 | 2.3 | 1099 | 4 | US-08-961-527-272 | Sequence 272, App | 661 | 14 | 2.3 | 1485 | 4 | US-08-936-165A-218 | Sequence 218, App |
| 589 | 14 | 2.3 | 1102 | 2 | US-08-133-990A-1 | Sequence 1, Appli | 662 | 14 | 2.3 | 1513 | 4 | US-09-686-583B-39 | Sequence 39, Appl |
| 590 | 14 | 2.3 | 1102 | 5 | PCT-US92-09382-1 | Sequence 1, Appli | C 663 | 14 | 2.3 | 1513 | 4 | US-09-686-583B-41 | Sequence 41, Appl |
| 591 | 14 | 2.3 | 1109 | 3 | US-09-352-990-5 | Sequence 5, Appli | C 664 | 14 | 2.3 | 1514 | 3 | US-08-675-816-1 | Sequence 1, Appli |
| 592 | 14 | 2.3 | 1110 | 4 | US-09-252-991A-1014 | Sequence 1014, Ap | 665 | 14 | 2.3 | 1522 | 2 | US-08-481-658B-1 | Sequence 1, Appli |
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| 594 | 14 | 2.3 | 1116 | 3 | US-09-345-603-3 | Sequence 3, Appli | 667 | 14 | 2.3 | 1522 | 2 | US-08-486-756A-1 | Sequence 1, Appli |
| 595 | 14 | 2.3 | 1116 | 4 | US-09-252-991A-3059 | Sequence 3059, Ap | 668 | 14 | 2.3 | 1522 | 2 | US-08-485-862B-1 | Sequence 1, Appli |
| 596 | 14 | 2.3 | 1119 | 3 | US-08-918-249-1 | Sequence 1, Appli | 669 | 14 | 2.3 | 1522 | 3 | US-08-787-739-1 | Sequence 1, Appli |
| 597 | 14 | 2.3 | 1119 | 3 | US-09-345-603-1 | Sequence 1, Appli | 670 | 14 | 2.3 | 1522 | 3 | US-08-487-077A-1 | Sequence 1, Appli |
| 598 | 14 | 2.3 | 1119 | 4 | US-09-328-352-1504 | Sequence 1504, Ap | 671 | 14 | 2.3 | 1522 | 3 | US-08-485-863A-1 | Sequence 1, Appli |
| 599 | 14 | 2.3 | 1125 | 4 | US-09-134-001C-2714 | Sequence 2714, Ap | 672 | 14 | 2.3 | 1522 | 3 | US-08-485-049D-1 | Sequence 1, Appli |
| 600 | 14 | 2.3 | 1128 | 4 | US-09-601-198-107 | Sequence 107, App | 673 | 14 | 2.3 | 1522 | 3 | US-09-178-115-1 | Sequence 1, Appli |
| 601 | 14 | 2.3 | 1129 | 4 | US-09-227-357-40 | Sequence 40, Appl | 674 | 14 | 2.3 | 1522 | 3 | US-09-177-776-1 | Sequence 1, Appli |
| 602 | 14 | 2.3 | 1137 | 6 | 5171843-8 | Parent No. 5171843 | 675 | 14 | 2.3 | 1522 | 4 | US-09-620-312D-96 | Sequence 96, Appl |
| 603 | 14 | 2.3 | 1146 | 3 | US-09-277-716-21 | Sequence 21, Appl | 676 | 14 | 2.3 | 1524 | 4 | US-09-134-001C-1141 | Sequence 1141, Ap |
| 604 | 14 | 2.3 | 1146 | 3 | US-09-609-161B-21 | Sequence 21, Appl | 677 | 14 | 2.3 | 1530 | 4 | US-09-328-352-739 | Sequence 739, App |
| 605 | 14 | 2.3 | 1152 | 4 | US-09-134-001C-592 | Sequence 592, App | 678 | 14 | 2.3 | 1532 | 3 | US-09-118-324-1 | Sequence 1, Appli |
| 606 | 14 | 2.3 | 1155 | 4 | US-09-252-991A-7856 | Sequence 7856, Ap | 679 | 14 | 2.3 | 1566 | 4 | US-09-134-001C-1453 | Sequence 1453, Ap |
| 607 | 14 | 2.3 | 1156 | 4 | US-09-620-312D-102 | Sequence 102, App | 680 | 14 | 2.3 | 1579 | 4 | US-09-591-095-9 | Sequence 9, Appli |
| 608 | 14 | 2.3 | 1188 | 4 | US-09-134-001C-886 | Sequence 886, App | 681 | 14 | 2.3 | 1586 | 4 | US-09-345-473B-1 | Sequence 1, Appli |
| 609 | 14 | 2.3 | 1189 | 2 | US-08-450-042A-2 | Sequence 2, Appli | 682 | 14 | 2.3 | 1606 | 4 | US-09-620-312D-99 | Sequence 99, Appl |
| 610 | 14 | 2.3 | 1212 | 2 | US-08-449-933-5 | Sequence 5, Appli | C 683 | 14 | 2.3 | 1610 | 2 | US-08-540-804-17 | Sequence 17, Appl |
| 611 | 14 | 2.3 | 1212 | 3 | US-07-966-049A-5 | Sequence 5, Appli | C 684 | 14 | 2.3 | 1610 | 2 | US-08-218-265-17 | Sequence 17, Appl |

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| C 685 | 14 | 2.3 | 1610 | 3 | US-08-521-872-17 | Sequence 17, Appl | 758 | 14 | 2.3 | 2156 | 4 | US-09-911-888-16 | Sequence 16, Appl |
| C 686 | 14 | 2.3 | 1610 | 3 | US-08-590-399-17 | Sequence 17, Appl | C 759 | 14 | 2.3 | 2156 | 4 | US-09-911-888-18 | Sequence 18, Appl |
| C 687 | 14 | 2.3 | 1615 | 2 | US-08-491-988-15 | Sequence 15, Appl | C 760 | 14 | 2.3 | 2157 | 2 | US-08-132-998A-7 | Sequence 7, Appl |
| C 688 | 14 | 2.3 | 1621 | 4 | US-09-227-357-29 | Sequence 29, Appl | C 761 | 14 | 2.3 | 2157 | 5 | PCT-US92-09382-7 | Sequence 7, Appl |
| C 689 | 14 | 2.3 | 1624 | 4 | US-08-491-988-14 | Sequence 14, Appl | C 762 | 14 | 2.3 | 2170 | 4 | US-09-172-339-1 | Sequence 21, Appl |
| C 690 | 14 | 2.3 | 1635 | 5 | PCT-US94-05795-11 | Sequence 11, Appl | C 763 | 14 | 2.3 | 2170 | 4 | US-09-398-395A-21 | Sequence 21, Appl |
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| C 692 | 14 | 2.3 | 1637 | 5 | PCT-US93-05704-3 | Sequence 3, Appl | C 765 | 14 | 2.3 | 2170 | 4 | US-09-895-752-21 | Sequence 21, Appl |
| C 693 | 14 | 2.3 | 1640 | 3 | US-08-781-250-1 | Sequence 1, Appl | C 766 | 14 | 2.3 | 2170 | 4 | US-09-903-012B-21 | Sequence 21, Appl |
| C 694 | 14 | 2.3 | 1648 | 2 | US-08-491-988-13 | Sequence 13, Appl | C 767 | 14 | 2.3 | 2182 | 2 | US-08-846-528-8 | Sequence 8, Appl |
| C 695 | 14 | 2.3 | 1662 | 4 | US-09-504-358-5 | Sequence 5, Appl | C 768 | 14 | 2.3 | 2193 | 3 | US-09-398-865A-1 | Sequence 1, Appl |
| C 696 | 14 | 2.3 | 1662 | 4 | US-09-554-314-5 | Sequence 4, Appl | C 769 | 14 | 2.3 | 2193 | 4 | US-09-710-714-1 | Sequence 1, Appl |
| C 697 | 14 | 2.3 | 1689 | 1 | US-07-991-867B-41 | Sequence 41, Appl | C 770 | 14 | 2.3 | 2213 | 4 | US-09-620-312D-799 | Sequence 799, App |
| C 698 | 14 | 2.3 | 1689 | 2 | US-08-544-332-41 | Sequence 41, Appl | C 771 | 14 | 2.3 | 2238 | 2 | US-08-919-624-2 | Sequence 2, Appl |
| C 699 | 14 | 2.3 | 1689 | 2 | US-09-370-861A-41 | Sequence 41, Appl | C 772 | 14 | 2.3 | 2238 | 2 | US-08-852-824-1 | Sequence 2, Appl |
| C 700 | 14 | 2.3 | 1689 | 2 | US-09-370-861A-41 | Sequence 41, Appl | C 773 | 14 | 2.3 | 2238 | 2 | US-08-852-824-1 | Sequence 2, Appl |
| C 701 | 14 | 2.3 | 1696 | 4 | US-08-961-527-297 | Sequence 297, App | C 774 | 14 | 2.3 | 2295 | 1 | US-08-375-300-3 | Sequence 1, Appl |
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| C 704 | 14 | 2.3 | 1713 | 4 | US-08-759-436-1 | Sequence 549, App | C 777 | 14 | 2.3 | 2340 | 4 | US-09-450-852-3 | Sequence 3, Appl |
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| C 707 | 14 | 2.3 | 1725 | 4 | US-08-842-248A-15 | Sequence 15, Appl | C 780 | 14 | 2.3 | 2359 | 1 | US-08-426-169-5 | Sequence 5, Appl |
| C 708 | 14 | 2.3 | 1733 | 3 | US-09-147-522-1 | Sequence 1, Appl | C 781 | 14 | 2.3 | 2359 | 3 | US-09-233-813-5 | Sequence 5, Appl |
| C 709 | 14 | 2.3 | 1737 | 4 | US-09-173-151A-1 | Sequence 3, Appl | C 782 | 14 | 2.3 | 2359 | 5 | PCT-US95-09470-5 | Sequence 5, Appl |
| C 710 | 14 | 2.3 | 1745 | 4 | US-09-388-349-5 | Sequence 5, Appl | C 783 | 14 | 2.3 | 2389 | 3 | US-08-961-083-55 | Sequence 55, Appl |
| C 711 | 14 | 2.3 | 1745 | 4 | US-09-388-349-5 | Sequence 5, Appl | C 784 | 14 | 2.3 | 2389 | 4 | US-09-536-784-55 | Sequence 55, Appl |
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| C 715 | 14 | 2.3 | 1785 | 4 | US-09-601-198-156 | Sequence 156, App | C 788 | 14 | 2.3 | 2410 | 2 | US-08-780-835B-1 | Sequence 1, Appl |
| C 716 | 14 | 2.3 | 1812 | 4 | US-09-268-347-37 | Sequence 37, Appl | C 789 | 14 | 2.3 | 2410 | 3 | US-09-303-268-1 | Sequence 1, Appl |
| C 717 | 14 | 2.3 | 1832 | 4 | US-09-686-583B-42 | Sequence 42, Appl | C 790 | 14 | 2.3 | 2410 | 3 | US-09-116-049-1 | Sequence 1, Appl |
| C 718 | 14 | 2.3 | 1832 | 4 | US-09-686-583B-44 | Sequence 44, Appl | C 791 | 14 | 2.3 | 2410 | 4 | US-09-884-363-1 | Sequence 1, Appl |
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| C 725 | 14 | 2.3 | 1926 | 2 | US-08-463-772-5 | Sequence 5, Appl | C 798 | 14 | 2.3 | 2501 | 3 | US-09-177-776-58 | Sequence 58, Appl |
| C 726 | 14 | 2.3 | 1926 | 5 | PCT-US93-05000-5 | Sequence 5, Appl | C 799 | 14 | 2.3 | 2521 | 4 | US-09-620-312D-777 | Sequence 777, App |
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| C 730 | 14 | 2.3 | 1984 | 1 | US-07-885-970A-25 | Sequence 25, Appl | C 803 | 14 | 2.3 | 2612 | 3 | US-09-042-785A-3 | Sequence 3, Appl |
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| C 733 | 14 | 2.3 | 1985 | 1 | US-08-298-687A-25 | Sequence 25, Appl | C 806 | 14 | 2.3 | 2640 | 1 | US-08-216-971-1 | Sequence 1, Appl |
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| C 737 | 14 | 2.3 | 2012 | 1 | US-08-478-992-3 | Sequence 3, Appl | C 810 | 14 | 2.3 | 2699 | 4 | US-09-336-115C-3 | Sequence 3, Appl |
| C 738 | 14 | 2.3 | 2012 | 3 | US-09-105-298-3 | Sequence 7, Appl | C 811 | 14 | 2.3 | 2722 | 2 | US-08-500-857A-7 | Sequence 7, Appl |
| C 739 | 14 | 2.3 | 2012 | 3 | US-08-706-281A-7 | Sequence 7, Appl | C 812 | 14 | 2.3 | 2739 | 4 | US-08-187-534A-1C | Sequence 156, App |
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| C 741 | 14 | 2.3 | 2012 | 4 | US-09-542-122-3 | Sequence 3, Appl | C 814 | 14 | 2.3 | 2799 | 4 | US-09-443-184-4-16 | Sequence 36, Appl |
| C 742 | 14 | 2.3 | 2037 | 3 | US-09-353-099-7 | Sequence 14, Appl | C 815 | 14 | 2.3 | 2821 | 4 | US-09-527-431-4-4 | Sequence 44, Appl |
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| C 745 | 14 | 2.3 | 2065 | 3 | US-08-335-865D-8 | Sequence 8, Appl | C 818 | 14 | 2.3 | 2859 | 3 | US-08-246-489-1 | Sequence 1, Appl |
| C 746 | 14 | 2.3 | 2073 | 4 | US-09-321-017B-894 | Sequence 894, App | C 819 | 14 | 2.3 | 2862 | 4 | US-09-328-352-1485 | Sequence 1485, Ap |
| C 747 | 14 | 2.3 | 2079 | 4 | US-09-268-347-25 | Sequence 25, Appl | C 820 | 14 | 2.3 | 2880 | 4 | US-09-443-184-4-16 | Sequence 36, Appl |
| C 748 | 14 | 2.3 | 2116 | 4 | US-09-180-852-1 | Sequence 1, Appl | C 821 | 14 | 2.3 | 2887 | 3 | US-09-016-434-1125 | Sequence 1125, Ap |
| C 749 | 14 | 2.3 | 2116 | 4 | US-09-484-970B-122 | Sequence 122, App | C 822 | 14 | 2.3 | 2906 | 4 | US-09-183-253-1 | Sequence 1, Appl |
| C 750 | 14 | 2.3 | 2126 | 4 | US-09-134-001C-2519 | Sequence 2519, Ap | C 823 | 14 | 2.3 | 2906 | 4 | US-09-996-243-500 | Sequence 500, App |
| C 751 | 14 | 2.3 | 2126 | 2 | US-08-545-745-1 | Sequence 1, Appl | C 824 | 14 | 2.3 | 2907 | 3 | US-08-816-346-1 | Sequence 1, Appl |
| C 752 | 14 | 2.3 | 2143 | 4 | US-09-328-352-424 | Sequence 424, App | C 825 | 14 | 2.3 | 2907 | 3 | US-08-816-346-55 | Sequence 55, Appl |
| C 753 | 14 | 2.3 | 2143 | 4 | US-09-205-258-235 | Sequence 235, App | C 826 | 14 | 2.3 | 2907 | 3 | US-09-335-411-1 | Sequence 1, Appl |
| C 754 | 14 | 2.3 | 2156 | 4 | US-08-965-762-16 | Sequence 16, Appl | C 827 | 14 | 2.3 | 2920 | 4 | US-09-335-411-55 | Sequence 55, Appl |
| C 755 | 14 | 2.3 | 2156 | 4 | US-09-911-927-16 | Sequence 16, Appl | C 828 | 14 | 2.3 | 2920 | 4 | US-09-620-312D-1084 | Sequence 1084, Ap |
| C 756 | 14 | 2.3 | 2156 | 4 | US-09-911-927-18 | Sequence 18, Appl | C 829 | 14 | 2.3 | 3001 | 4 | US-09-539-333D-129 | Sequence 129, App |
| C 757 | 14 | 2.3 | 2156 | 4 | US-09-911-882-16 | Sequence 16, Appl | C 830 | 14 | 2.3 | 3001 | 4 | US-09-539-333D-184 | Sequence 184, App |
| C 757 | 14 | 2.3 | 2156 | 4 | US-09-911-882-18 | Sequence 18, Appl | | | | | | US-09-539-333D-195 | Sequence 195, App |

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| 831 | 14 | 2.3 | 3001 | 4 | US-09-539-333D-199 | Sequence 199, App | C 904 | 14 | 2.3 | 3834 | 4 | US-09-620-312D-933 | Sequence 933, App |
| 832 | 14 | 2.3 | 3030 | 4 | US-09-268-347-29 | Sequence 29, Appl | 905 | 14 | 2.3 | 3865 | 1 | US-08-832-883-48 | Sequence 48, Appl |
| C 833 | 14 | 2.3 | 3032 | 4 | US-08-990-140-1 | Sequence 1, Appl | C 906 | 14 | 2.3 | 3865 | 1 | US-08-832-883-48 | Sequence 48, Appl |
| C 834 | 14 | 2.3 | 3032 | 4 | US-09-546-238-1 | Sequence 1, Appl | C 907 | 14 | 2.3 | 3865 | 2 | US-08-832-877-48 | Sequence 48, Appl |
| 835 | 14 | 2.3 | 3036 | 4 | US-09-268-347-23 | Sequence 23, Appl | C 908 | 14 | 2.3 | 3865 | 2 | US-08-832-877-48 | Sequence 48, Appl |
| 836 | 14 | 2.3 | 3063 | 4 | US-08-184-009-169 | Sequence 169, App | 909 | 14 | 2.3 | 3967 | 2 | US-08-821-994-72 | Sequence 72, Appl |
| 837 | 14 | 2.3 | 3063 | 2 | US-08-458-356-169 | Sequence 169, App | 910 | 14 | 2.3 | 4016 | 1 | US-08-410-540-3 | Sequence 3, Appl |
| 838 | 14 | 2.3 | 3063 | 4 | US-08-460-736-169 | Sequence 169, App | C 911 | 14 | 2.3 | 4035 | 4 | US-09-016-434-1369 | Sequence 1369, App |
| 839 | 14 | 2.3 | 3063 | 4 | US-09-535-370-169 | Sequence 169, App | C 912 | 14 | 2.3 | 4080 | 1 | US-08-375-300-1 | Sequence 1, Appl |
| 840 | 14 | 2.3 | 3115 | 4 | US-09-702-705-802 | Sequence 802, App | C 913 | 14 | 2.3 | 4080 | 3 | US-09-177-431-1 | Sequence 1, Appl |
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| 842 | 14 | 2.3 | 3129 | 4 | US-09-904-615-18 | Sequence 18, Appl | 915 | 14 | 2.3 | 4104 | 3 | US-08-881-706-1 | Sequence 1, Appl |
| 843 | 14 | 2.3 | 3144 | 4 | US-08-961-527-224 | Sequence 224, App | 916 | 14 | 2.3 | 4138 | 1 | US-08-447-411-15 | Sequence 75, Appl |
| 844 | 14 | 2.3 | 3162 | 4 | US-09-221-017B-766 | Sequence 766, App | 917 | 14 | 2.3 | 4138 | 2 | US-08-662-227-33 | Sequence 33, Appl |
| 845 | 14 | 2.3 | 3165 | 4 | US-09-601-198-102 | Sequence 102, App | 918 | 14 | 2.3 | 4138 | 4 | US-09-017-947-33 | Sequence 33, Appl |
| C 846 | 14 | 2.3 | 3177 | 4 | US-09-601-198-102 | Sequence 102, App | C 919 | 14 | 2.3 | 4148 | 4 | US-09-435-019-13 | Sequence 13, Appl |
| C 847 | 14 | 2.3 | 3177 | 3 | US-09-134-513-1 | Sequence 1, Appl | C 920 | 14 | 2.3 | 4148 | 4 | US-09-435-019-15 | Sequence 15, Appl |
| C 848 | 14 | 2.3 | 3191 | 3 | US-08-675-816-3 | Sequence 3, Appl | C 921 | 14 | 2.3 | 4160 | 4 | US-09-134-218-1 | Sequence 1, Appl |
| C 849 | 14 | 2.3 | 3195 | 4 | US-09-527-058-3 | Sequence 3, Appl | 922 | 14 | 2.3 | 4161 | 4 | US-09-252-991A-12016 | Sequence 12016, A |
| C 850 | 14 | 2.3 | 3245 | 1 | US-07-935-311A-3 | Sequence 3, Appl | C 923 | 14 | 2.3 | 4203 | 2 | US-08-288-630-3 | Sequence 3, Appl |
| C 851 | 14 | 2.3 | 3245 | 1 | US-08-368-079-3 | Sequence 3, Appl | C 924 | 14 | 2.3 | 4223 | 3 | US-09-541-782-5 | Sequence 5, Appl |
| C 852 | 14 | 2.3 | 3245 | 5 | PCT-US93-07996-3 | Sequence 3, Appl | C 925 | 14 | 2.3 | 4223 | 3 | US-09-723-820-5 | Sequence 5, Appl |
| C 853 | 14 | 2.3 | 3300 | 4 | US-09-336-643A-82 | Sequence 82, Appl | C 926 | 14 | 2.3 | 4228 | 3 | US-08-678-614-1 | Sequence 1, Appl |
| C 854 | 14 | 2.3 | 3300 | 4 | US-09-620-312D-456 | Sequence 456, App | C 927 | 14 | 2.3 | 4285 | 4 | US-09-410-464-1 | Sequence 1, Appl |
| C 855 | 14 | 2.3 | 3312 | 4 | US-09-601-198-58 | Sequence 58, App | 928 | 14 | 2.3 | 4301 | 4 | US-08-121-446-3 | Sequence 3, Appl |
| C 856 | 14 | 2.3 | 3331 | 3 | US-08-864-038A-2 | Sequence 2, Appl | C 929 | 14 | 2.3 | 4398 | 1 | US-08-961-527-293 | Sequence 293, App |
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| C 858 | 14 | 2.3 | 3340 | 4 | US-09-021-560-1 | Sequence 1, Appl | C 931 | 14 | 2.3 | 4443 | 4 | US-09-425-453A-1 | Sequence 1, Appl |
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| C 865 | 14 | 2.3 | 3426 | 3 | US-08-654-025-6 | Sequence 6, Appl | C 938 | 14 | 2.3 | 4443 | 4 | US-09-425-453A-15 | Sequence 15, Appl |
| C 866 | 14 | 2.3 | 3460 | 4 | US-09-620-312D-666 | Sequence 666, App | C 939 | 14 | 2.3 | 4443 | 4 | US-09-425-453A-17 | Sequence 17, Appl |
| C 867 | 14 | 2.3 | 3465 | 4 | US-09-134-001C-591 | Sequence 591, App | C 940 | 14 | 2.3 | 4443 | 4 | US-09-425-453A-19 | Sequence 19, Appl |
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| 871 | 14 | 2.3 | 3507 | 1 | US-08-315-468-3 | Sequence 3, Appl | C 944 | 14 | 2.3 | 4576 | 2 | US-08-832-877-49 | Sequence 49, Appl |
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| 874 | 14 | 2.3 | 3520 | 1 | US-08-110-683-3 | Sequence 3, Appl | C 947 | 14 | 2.3 | 4712 | 4 | US-09-221-017B-577 | Sequence 577, App |
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| 876 | 14 | 2.3 | 3520 | 2 | US-08-472-097-3 | Sequence 3, Appl | C 949 | 14 | 2.3 | 4874 | 4 | US-09-484-970B-36 | Sequence 36, Appl |
| 877 | 14 | 2.3 | 3520 | 2 | US-09-439-672-3 | Sequence 3, Appl | C 950 | 14 | 2.3 | 4875 | 1 | US-08-460-739-1 | Sequence 1, Appl |
| 878 | 14 | 2.3 | 3520 | 5 | PCT-US93-11638-3 | Sequence 3, Appl | C 951 | 14 | 2.3 | 4895 | 4 | US-09-426-568A-3 | Sequence 3, Appl |
| 879 | 14 | 2.3 | 3532 | 3 | US-08-787-733-90 | Sequence 90, Appl | C 952 | 14 | 2.3 | 4935 | 2 | US-08-631-097-3 | Sequence 5, Appl |
| 880 | 14 | 2.3 | 3532 | 3 | US-09-178-115-90 | Sequence 90, Appl | C 953 | 14 | 2.3 | 4951 | 2 | US-08-867-030B-5 | Sequence 5, Appl |
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| 882 | 14 | 2.3 | 3534 | 4 | US-09-134-001C-2269 | Sequence 2269, App | C 955 | 14 | 2.3 | 4970 | 1 | US-08-764-100-14 | Sequence 14, Appl |
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| C 884 | 14 | 2.3 | 3551 | 2 | US-08-870-693-18 | Sequence 18, Appl | C 957 | 14 | 2.3 | 5011 | 1 | US-08-141-893-1 | Sequence 1, Appl |
| C 885 | 14 | 2.3 | 3562 | 4 | US-09-068-506-2 | Sequence 2, Appl | C 958 | 14 | 2.3 | 5011 | 1 | US-08-463-092B-1 | Sequence 1, Appl |
| C 886 | 14 | 2.3 | 3633 | 4 | US-09-221-017B-362 | Sequence 362, App | C 959 | 14 | 2.3 | 5011 | 1 | US-08-463-092B-3 | Sequence 3, Appl |
| 887 | 14 | 2.3 | 3636 | 4 | US-09-328-352-3841 | Sequence 3841, App | C 960 | 14 | 2.3 | 5011 | 2 | US-08-462-109A-1 | Sequence 1, Appl |
| C 888 | 14 | 2.3 | 3690 | 4 | US-09-016-434-1234 | Sequence 1234, App | C 961 | 14 | 2.3 | 5011 | 2 | US-08-462-109A-3 | Sequence 3, Appl |
| C 889 | 14 | 2.3 | 3701 | 3 | US-08-845-258-10 | Sequence 10, Appl | C 962 | 14 | 2.3 | 5011 | 2 | US-08-460-907B-1 | Sequence 1, Appl |
| C 890 | 14 | 2.3 | 3701 | 3 | US-08-990-571-10 | Sequence 10, Appl | C 963 | 14 | 2.3 | 5011 | 2 | US-08-460-907B-3 | Sequence 3, Appl |
| C 891 | 14 | 2.3 | 3701 | 4 | US-08-723-142A-10 | Sequence 10, Appl | C 964 | 14 | 2.3 | 5011 | 3 | US-08-463-179A-1 | Sequence 1, Appl |
| C 892 | 14 | 2.3 | 3701 | 4 | US-09-528-784A-10 | Sequence 10, Appl | C 965 | 14 | 2.3 | 5011 | 3 | US-08-463-179A-3 | Sequence 3, Appl |
| C 893 | 14 | 2.3 | 3701 | 4 | US-09-583-545-1 | Sequence 1, Appl | C 966 | 14 | 2.3 | 5011 | 3 | US-08-461-384B-1 | Sequence 1, Appl |
| 894 | 14 | 2.3 | 3701 | 4 | US-09-617-594A-5 | Sequence 5, Appl | C 967 | 14 | 2.3 | 5011 | 3 | US-08-461-384B-3 | Sequence 3, Appl |
| C 895 | 14 | 2.3 | 3701 | 4 | US-09-569-098A-50 | Sequence 50, Appl | C 968 | 14 | 2.3 | 5011 | 3 | US-08-407-207A-1 | Sequence 1, Appl |
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| C 900 | 14 | 2.3 | 3718 | 4 | US-09-424-283-6 | Sequence 63, Appl | 973 | 14 | 2.3 | 5222 | 4 | US-09-336-946B-68 | Sequence 68, Appl |
| 901 | 14 | 2.3 | 3791 | 4 | US-09-149-476-216 | Sequence 216, App | 974 | 14 | 2.3 | 5240 | 4 | US-09-171-337A-2 | Sequence 2, Appl |
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| C 903 | 14 | 2.3 | 3812 | 1 | US-08-646-715-19 | Sequence 19, Appl | C 976 | 14 | 2.3 | 5261 | 1 | US-08-045-806-3 | Sequence 3, Appl |

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C 977 14 2.3 5261 1 US-08-366-051B-3 Sequence 3, App11
C 978 14 2.3 5303 4 US-08-971-395-4 Sequence 4, App1
C 979 14 2.3 5305 4 US-08-961-527-135 Sequence 135, App
C 980 14 2.3 5401 3 US-09-269-040-1 Sequence 1, App11
C 981 14 2.3 5407 3 US-09-269-040-7 Sequence 7, App11
C 982 14 2.3 5416 4 US-09-284-926-8 Sequence 8, App11
C 983 14 2.3 5433 3 US-08-929-329-1 Sequence 1, App11
C 984 14 2.3 5433 2 US-08-687-080-101 Sequence 101, App
C 985 14 2.3 5574 1 US-08-450-257-22 Sequence 22, App1
C 986 14 2.3 5574 1 US-08-450-246-22 Sequence 22, App1
C 987 14 2.3 5574 1 US-08-450-098-22 Sequence 22, App1
C 988 14 2.3 5574 1 US-08-451-233-22 Sequence 22, App1
C 989 14 2.3 5574 1 US-08-450-236-22 Sequence 22, App1
C 990 14 2.3 5574 4 US-08-235-403-22 Sequence 22, App1
C 991 14 2.3 5581 4 US-08-973-544-1 Sequence 1, App11
C 992 14 2.3 5635 3 US-08-136-742A-3 Sequence 3, App11
C 993 14 2.3 5635 3 US-09-248-026-3 Sequence 3, App11
C 994 14 2.3 5635 5 PCT-US93-11667-3 Sequence 3, App11
C 995 14 2.3 5706 4 US-09-738-946-11 Sequence 11, App1
C 996 14 2.3 5757 4 US-09-336-946B-1 Sequence 1, App11
C 997 14 2.3 5886 3 US-08-810-712-9 Sequence 9, App11
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C 999 14 2.3 5977 3 US-09-024-020B-1 Sequence 1, App11
C1000 14 2.3 5977 4 US-09-425-043-1 Sequence 1, App11
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ALIGNMENTS

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RESULT 1
US-09-495-050A-28
; Sequence 28, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 647628CT1
US-09-495-050A-28

Query Match 3.1%; Score 19; DB 4; Length 948;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 ACCTATTTTATGATGCCA 279
Db 678 ACCTATTTTATGATGCCA 696

RESULT 2
US-09-422-978-2313/c
; Sequence 2313, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
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; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2313
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-10364-331 : polymorphic base A or G
US-09-422-978-2313

Query Match 2.9%; Score 18; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 TTTGAAACAATTTCTA 179
Db 21 TTTGAAACAATTTCTA 4
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RESULT 3
US-08-232-463-29/c
; Sequence 29, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: oligonucleotide II
US-08-232-463-29

Query Match 2.9%; Score 18; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
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Db 35 TTCTACTATATTTTACA 18

RESULT 4

US-08-232-463-38/c
Sequence 38, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: sp11 (4)
US-08-232-463-38

Query Match 2.9%; Score 18; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
|||||
Db 35 TTCTACTATATTTTACA 18

RESULT 5

US-08-232-463-44/c
Sequence 44, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: Plim
US-08-232-463-44

Query Match 2.9%; Score 18; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
|||||
Db 34 TTCTACTATATTTTACA 17

RESULT 6

US-08-232-463-45/c
Sequence 45, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA

```
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: SP11
US-08-232-463-45
```

```
Query Match      2.9% Score 18; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      175 TTCTACTATATTTTACA 192
Db      35 TTCTACTATATTTTACA 18
```

```
RESULT 7
US-08-232-463-43/c
Sequence 43, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
```

```
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: P11wc
US-08-232-463-43
```

```
Query Match      2.9% Score 18; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      175 TTCTACTATATTTTACA 192
Db      29 TTCTACTATATTTTACA 12
```

```
RESULT 8
US-09-439-313-535/c
Sequence 535, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-535
```

```
Query Match      2.9% Score 18; DB 4; Length 6082;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      114 AGCAGGATGCTGGGGCT 131
Db      107 AGCAGGATGCTGGGGCT 90
```

```
RESULT 9
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
```


TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpc-Fls
US-08-232-463-14

Query Match 2.9%; Score 18; DB 1; Length 7218;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTCTACTATATTTTACA 192
|||||
DB 1599 TTCTACTATATTTTACA 1582

RESULT 10
US-08-232-463-2/c
Sequence 2, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTKm-sp11
US-08-232-463-2

Query Match 2.9%; Score 18; DB 1; Length 8313;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTCTACTATATTTTACA 192
|||||
DB 4160 TTCTACTATATTTTACA 4143

RESULT 11
US-08-480-882B-3
Sequence 3, Application US/08480882B
Patent No. 5656275
GENERAL INFORMATION:
APPLICANT: WASKOEN, TERRI
APPLICANT: CHAVEZ, LLOYD
APPLICANT: CHU, HSIEN-JUE
TITLE OF INVENTION: RECOMBINANT RACCOON FOX VIRUSES
TITLE OF INVENTION: AND THEIR USE AS AN EFFECTIVE VACCINE AGAINST FELINE
TITLE OF INVENTION: INFECTIOUS PERITONITIS VIRUS DISEASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Darby & Darby, P.C.
STREET: 805 Third Avenue 27th Floor
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,882B
FILING DATE: 07-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,516
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 0632/08669
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2125277700
TELEFAX: 2127536237

TELEX: 236687
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8710 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Feline infectious peritonitis virus
IMMEDIATE SOURCE:
CLONE: psc11f1
US-08-480-882B-3

Query Match 2.9%; Score 18; DB 1; Length 8710;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
|||||
Db 6148 TTCTACTATATTTTACA 6165

RESULT 12
US-08-480-210-3
Sequence 3, Application US/08480210
Patent No. 5770211
GENERAL INFORMATION:
APPLICANT: MASMOEN, TERRI
APPLICANT: CHAVEZ, LLOYD
APPLICANT: CHU, HSIEN-JUE
TITLE OF INVENTION: RECOMBINANT RACCOON POX VIRUSES
TITLE OF INVENTION: AND THEIR USE AS AN EFFECTIVE VACCINE AGAINST FELINE
TITLE OF INVENTION: INFECTIOUS PERITONITIS VIRUS DISEASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
STREET: 805 Third Avenue 27th Floor
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,210
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,516
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 0632/18669-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2125277700
TELEFAX: 2127536237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8710 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Feline infectious peritonitis virus
IMMEDIATE SOURCE:
CLONE: psc11f1

US-08-480-210-3

Query Match 2.9%; Score 18; DB 1; Length 8710;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
|||||
Db 6148 TTCTACTATATTTTACA 6165

RESULT 13
US-08-480-882B-4
Sequence 4, Application US/08480882B
Patent No. 5556275
GENERAL INFORMATION:
APPLICANT: MASMOEN, TERRI
APPLICANT: CHAVEZ, LLOYD
APPLICANT: CHU, HSIEN-JUE
TITLE OF INVENTION: RECOMBINANT RACCOON POX VIRUSES
TITLE OF INVENTION: AND THEIR USE AS AN EFFECTIVE VACCINE AGAINST FELINE
TITLE OF INVENTION: INFECTIOUS PERITONITIS VIRUS DISEASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
STREET: 805 Third Avenue 27th Floor
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,882B
FILING DATE: 07-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,516
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 0632/08669
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2125277700
TELEFAX: 2127536237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 9019 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Feline immunodeficiency virus
IMMEDIATE SOURCE:
CLONE: psc11e1
US-08-480-882B-4

Query Match 2.9%; Score 18; DB 1; Length 9019;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
|||||
Db 6147 TTCTACTATATTTTACA 6164

RESULT 14

US-08-480-210-4
; Sequence 4, Application US/08480210
; Patent No. 5770211
; GENERAL INFORMATION:
; APPLICANT: WASMOEN, TERRI
; APPLICANT: CHAVEZ, LLOYD
; APPLICANT: CHU, HSIEH-JUE
; TITLE OF INVENTION: RECOMBINANT RACCOON POX VIRUSES
; TITLE OF INVENTION: AND THEIR USE AS AN EFFECTIVE VACCINE AGAINST FELINE
; TITLE OF INVENTION: INSPECTIOUS PERITONITIS VIRUS DISEASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue 27th Floor
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,210
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/125,516
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0632/18669-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2125277700
; TELEFAX: 2127536237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9019 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Feline immunodeficiency virus
; IMMEDIATE SOURCE:
; CLONE: psc11e1
; US-08-480-210-4

Query Match 2.9%; Score 18; DB 1; Length 9019;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 175 TTCTACTATATTTTACA 192
|||
Db 6147 TTCTACTATATTTTACA 6164

RESULT 15
US-08-232-463-3/c
; Sequence 3, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHIEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9454 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTKm-VtkA
; US-08-232-463-3

Query Match 2.9%; Score 18; DB 1; Length 9454;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 175 TTCTACTATATTTTACA 192
|||
Db 5301 TTCTACTATATTTTACA 5284

RESULT 16
US-08-232-463-4/c
; Sequence 4, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHIEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313

FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 9454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTKm-VLkb
US-08-232-463-4

Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
Db 5301 TTCTACTATATTTTACA 5284

RESULT 17
US-08-232-463-16
Sequence 16, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 9917 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-spl1
US-08-232-463-16

Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
Db 4329 TTCTACTATATTTTACA 4346

RESULT 18
US-09-146-053-3/c
Sequence 3, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
EARLIER FILING DATE: 1998-09-02
CURRENT FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 50000
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-053-3

Query Match
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 495 AGAGTTTCAAACTTTT 512
Db 39492 AGAGTTTCAAACTTTT 39475

RESULT 19
US-09-733-294A-30
Sequence 30, Application US/09733294A
Patent No. 6492171
GENERAL INFORMATION:
APPLICANT: Brett P. Montia
APPLICANT: William Gaarde
APPLICANT: Susan M. Freiler
APPLICANT: Edward V. Manciewicz
TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
FILE REFERENCE: ISPH-0527
CURRENT APPLICATION NUMBER: US/09/733,294A
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/572,423
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 30
LENGTH: 51552
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: (1)...(11492)
OTHER INFORMATION: exon 1
NAME/KEY: intron
LOCATION: (11493)...(11596)
OTHER INFORMATION: intron 1

NAME/KEY: exon
 LOCATION: (11597)...(12950)
 OTHER INFORMATION: exon 2
 NAME/KEY: intron
 LOCATION: (12951)...(121566)
 OTHER INFORMATION: intron 2
 NAME/KEY: exon
 LOCATION: (21567)...(21762)
 OTHER INFORMATION: exon 3
 NAME/KEY: intron
 LOCATION: (21763)...(23851)
 OTHER INFORMATION: intron 3
 NAME/KEY: exon
 LOCATION: (23852)...(24032)
 OTHER INFORMATION: exon 4
 NAME/KEY: intron
 LOCATION: (24033)...(24719)
 OTHER INFORMATION: intron 4
 NAME/KEY: exon
 LOCATION: (24720)...(24899)
 OTHER INFORMATION: exon 5
 NAME/KEY: intron
 LOCATION: (24900)...(25393)
 OTHER INFORMATION: intron 5
 NAME/KEY: exon
 LOCATION: (25394)...(25549)
 OTHER INFORMATION: exon 6
 NAME/KEY: intron
 LOCATION: (25550)...(30196)
 OTHER INFORMATION: intron 6
 NAME/KEY: exon
 LOCATION: (30195)...(30292)
 OTHER INFORMATION: exon 7
 NAME/KEY: intron
 LOCATION: (30293)...(31272)
 OTHER INFORMATION: intron 7
 NAME/KEY: exon
 LOCATION: (31273)...(31358)
 OTHER INFORMATION: exon 8
 NAME/KEY: intron
 LOCATION: (31359)...(33843)
 OTHER INFORMATION: intron 8
 NAME/KEY: unsure
 LOCATION: 31450
 OTHER INFORMATION: unknown
 NAME/KEY: exon
 LOCATION: (33844)...(33957)
 OTHER INFORMATION: exon 9
 NAME/KEY: intron
 LOCATION: (33958)...(35941)
 OTHER INFORMATION: intron 9
 NAME/KEY: exon
 LOCATION: (35942)...(36013)
 OTHER INFORMATION: exon 10
 NAME/KEY: intron
 LOCATION: (36014)...(37884)
 OTHER INFORMATION: intron 10
 NAME/KEY: exon
 LOCATION: (37885)...(38073)
 OTHER INFORMATION: exon 11
 NAME/KEY: intron
 LOCATION: (38074)...(41874)
 OTHER INFORMATION: intron 11
 NAME/KEY: exon
 LOCATION: (41875)...(42001)
 OTHER INFORMATION: exon 12
 NAME/KEY: intron
 LOCATION: (42002)...(42881)
 OTHER INFORMATION: intron 12
 NAME/KEY: exon
 LOCATION: (42882)...(42943)
 OTHER INFORMATION: exon 13
 NAME/KEY: intron

LOCATION: (42944)...(46129)
 OTHER INFORMATION: intron 13
 NAME/KEY: exon
 LOCATION: (46130)...(46254)
 OTHER INFORMATION: exon 14
 NAME/KEY: intron
 LOCATION: (46255)...(47035)
 OTHER INFORMATION: intron 14
 NAME/KEY: exon
 LOCATION: (47036)...(47173)
 OTHER INFORMATION: exon 15
 NAME/KEY: intron
 LOCATION: (47174)...(47709)
 OTHER INFORMATION: intron 15
 NAME/KEY: exon
 LOCATION: (47710)...(50544)
 OTHER INFORMATION: exon 16
 US-09-733-294A-30

Query Match 2.9%; Score 18; DB 4; Length 51552;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 GCAGCAGGATGCTGGCG 129
 Db 48650 GCAGCAGGATGCTGGCG 48667

RESULT 20
 US-08-998-416-574
 Sequence 574, Application US/08998416
 Patent No. 6239264
 GENERAL INFORMATION:
 APPLICANT: Philippsen, Peter
 APPLICANT: Pohmann, Rainer
 APPLICANT: Steiner, Sabine
 APPLICANT: Mohr, Christine
 APPLICANT: Wendland, Jurgen
 APPLICANT: Knechtle, Philipp
 APPLICANT: Reibschung, Corinne
 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
 TITLE OF INVENTION: AND USES THEREOF
 NUMBER OF SEQUENCES: 1152
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6239264artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: No. 6239264th Carolina
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/998,416
 FILING DATE: 24-DEC-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: CH 0016/97
 FILING DATE: 31-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8587
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 574:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 753 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1397RP
US-08-998-416-574

Query Match 2.7%; Score 17; DB 3; Length 753;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 TATTATTATGATGCCA 280
DB 286 TATTATTATGATGCCA 302

RESULT 21

US-09-107-532A-2443
Sequence 2443; Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Daneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2443:
SEQUENCE CHARACTERISTICS:
LENGTH: 876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...876
SEQUENCE DESCRIPTION: SEQ ID NO: 2443:
US-09-107-532A-2443
Query Match 2.7%; Score 17; DB 4; Length 876;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 464 TAGGATGTTCCATAT 480
DB 617 TAGGATGTTCCATAT 633

RESULT 22

US-09-016-434-982
Sequence 982; Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
TELEFAX: (650) 855-0555
INFORMATION FOR SEQ ID NO: 982:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGA101
CLONE: 873352
US-09-016-434-982
Query Match 2.7%; Score 17; DB 4; Length 1337;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 TTTGAACAATTTCT 178
DB 406 TTTGAACAATTTCT 422

RESULT 23
US-09-329-633A-1
Sequence 1; Application US/09329633A
Patent No. 6252050
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntcharapai, Anan
APPLICANT: Kim, K. Jin
TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD
FILE REFERENCE: P1468R1 (REVISED)

;; CURRENT APPLICATION NUMBER: US/09/329,633A
;; CURRENT FILING DATE: 1999-06-10
;; PRIOR APPLICATION NUMBER: US 60/089,253
;; PRIOR FILING DATE: 1998-06-12
;; NUMBER OF SEQ ID NOS: 2
;; SEQ ID NO: 1
;; LENGTH: 1799
;; TYPE: DNA
;; ORGANISM: human
US-09-329-633A-1

Query Match 2.7%; Score 17; DB 3; Length 1799;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 230 ATGCTTATTATTAT 246
Db 1684 ATGCTTATTATTAT 1700

RESULT 24

US-09-079-029-2
; Sequence 2, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapal, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:

;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Marschang, Diane L.
;; REGISTRATION NUMBER: 35,600
;; REFERENCE/DOCKET NUMBER: P1101R2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-5416
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1799 base pairs
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
US-09-079-029-2

Query Match 2.7%; Score 17; DB 4; Length 1799;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 230 ATGCTTATTATTAT 246
Db 1684 ATGCTTATTATTAT 1700

RESULT 25

US-09-453-702B-188

;; Sequence 188, Application US/09453702B
;; Patent No. 6365723
;; GENERAL INFORMATION:
;; APPLICANT: Blatner, Frederick R.
;; Burland, Nicole T.
;; Perna, Nicole T.
;; Plunkett, Guy
;; Welch, Rod

;; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
;; NUMBER OF SEQUENCES: 265
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Quarles & Brady
;; STREET: 1 South Plinkney Street
;; CITY: Madison
;; STATE: WI
;; COUNTRY: US
;; ZIP: 53701-2113

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 8.0

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/453,702B
;; FILING DATE: 03-Dec-1999
;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/110,955
;; FILING DATE: 04-DEC-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seay, Nicholas J.
;; REGISTRATION NUMBER: 27386
;; REFERENCE/DOCKET NUMBER: 960296.95017

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (608) 251-5000
;; TELEFAX: (608) 251-9166
;; INFORMATION FOR SEQ ID NO: 188:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1819
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear

;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 188:
US-09-453-702B-188

Query Match 2.7%; Score 17; DB 4; Length 1819;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 159 TCATTGAAACATTT 175
Db 82 TCATTGAAACATTT 98

;; RESULT 26
;; US-08-915-795-4
;; Sequence 4, Application US/08915795
;; Patent No. 6235713
;; GENERAL INFORMATION:
;; APPLICANT: Marc G. ACHEN
;; APPLICANT: Andrew F. WILKS
;; APPLICANT: Steven A. STACKER

;; APPLICANT: Kari ALITALO
;; TITLE OF INVENTION: GROWTH FACTOR
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;; STREET: 1200 G Street, NW, Suite 700
;; CITY: Washington

;; STATE: DC
;; COUNTRY: United States of America
;; ZIP: 20005

```
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/915,795
/ FILING DATE:
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: EVANS, Joseph D.
/ REGISTRATION NUMBER: 26,269
/ REFERENCE/DOCKET NUMBER: 1064/42983
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 628-8800
/ TELEFAX: (202) 628-8844
/ TELEX: N/A
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2029 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ TISSUE TYPE: Human Lung
/ US-08-915-795-4
```

```
Query Match          2.7% Score 17; DB 3; Length 2029;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      162 TTTTGAACAATTCT 178
        |||||||
DB      341 TTTTGAACAATTCT 357
```

```
RESULT 27
US-09-134-001C-1659
/ Sequence 1659, Application US/09134001C
/ Patent No. 6380370
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/ FILE REFERENCE: GTC-007
/ CURRENT APPLICATION NUMBER: US/09/134,001C
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/064,964
/ PRIOR FILING DATE: 1997-11-08
/ PRIOR APPLICATION NUMBER: US 60/055,779
/ PRIOR FILING DATE: 1997-08-14
/ NUMBER OF SEQ ID NOS: 5674
/ SEQ ID NO 1659
/ LENGTH: 2661
/ TYPE: DNA
/ ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1659
```

```
Query Match          2.7% Score 17; DB 4; Length 2661;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      161 ATTTGAACAATTTC 177
        |||||||
DB      1835 ATTTGAACAATTTC 1851
```

```
RESULT 28
US-09-333-593A-1
/ Sequence 1, Application US/09333593A
/ Patent No. 6313269
```

```
/ GENERAL INFORMATION:
/ APPLICANT: DEEN, KEITH C.
/ APPLICANT: YOUNG, PETER R.
/ APPLICANT: MARSHALL, LISA A.
/ APPLICANT: ROSHAK, AMY K.
/ APPLICANT: TAN, KONG B.
/ TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR.
/ FILE REFERENCE: TR6
/ CURRENT APPLICATION NUMBER: US/09/333,593A
/ CURRENT FILING DATE: 1999-06-15
/ PRIOR APPLICATION NUMBER: 08/916,625
/ PRIOR FILING DATE: 1997-08-22
/ PRIOR APPLICATION NUMBER: 08/853,684
/ PRIOR FILING DATE: 1997-05-09
/ PRIOR APPLICATION NUMBER: 60/041,230
/ PRIOR FILING DATE: 1997-03-14
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 3881
/ TYPE: DNA
/ ORGANISM: HOMO SAPIENS
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (3538) (3598) (3601) (3607) (3608) (3619) (3632) (3659) (3686) (3690)
US-09-333-593A-1
```

```
Query Match          2.7% Score 17; DB 4; Length 3881;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      230 ATGCTTATTATTAT 246
        |||||||
DB      1638 ATGCTTATTATTAT 1654
```

```
RESULT 29
US-09-620-312D-156/C
/ Sequence 156, Application US/09620312D
/ Patent No. 6569682
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yundong
/ APPLICANT: Wang, Duntui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinghast
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 6569682e1 Nucleic Acids and
/ FILE REFERENCE: 784CIP28
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ CURRENT FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1105
/ SOFTWARE: pc_fl_genes Version 1.0
/ SEQ ID NO 156
/ LENGTH: 4053
```


TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (409)..(3819)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(4053)
OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-156

Query Match 2.7%; Score 17; DB 4; Length 4053;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 534 TTCAGTGTGCAGATT 550
DB 513 TTCAGTGTGCAGATT 497

RESULT 30

US-08-400-159-1/c
Sequence 1, Application US/08400159
Patent No. 5869282

GENERAL INFORMATION:

APPLICANT: Ish-Horowitz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,159
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 5561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 442..4656

US-08-400-159-1

Query Match 2.7%; Score 17; DB 2; Length 5561;

Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 373 AAATTATATATATAA 389
DB 5499 AAATTATATATATAA 5483

RESULT 31

US-08-611-729A-1/c
Sequence 1, Application US/08611729A
Patent No. 6004924

GENERAL INFORMATION:

APPLICANT: Ish-Horowitz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 5561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 442..4653

US-08-611-729A-1

Query Match 2.7%; Score 17; DB 3; Length 5561;

Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 373 AAATTATATATATAA 389
DB 5499 AAATTATATATATAA 5483

RESULT 32

US-08-961-527-198
Sequence 198, Application US/08961527
Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 331
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
LENGTH: 6846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-198

Query Match 2.7%; Score 17; DB 4; Length 6846;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 462 TATAGTATTGTTCCAT 478
|||||
DB 1806 TATAGTATTGTTCCAT 1822

RESULT 33
US-08-287-959-2
Sequence 2, Application US/08287959
Patent No. 5639651
GENERAL INFORMATION:
APPLICANT: Weisbach, Lawrence
APPLICANT: Bernards, Andre
APPLICANT: Settleman, Jeffrey
TITLE OF INVENTION: GAP-RELATED GENE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,959
FILING DATE: August 9, 1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/181001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7573 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-287-959-2

Query Match 2.7%; Score 17; DB 1; Length 7573;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 AGAGTACTATTAT 271
|||||
DB 280 AGAGTACTATTAT 296

RESULT 34
US-09-759-359A-3
Sequence 3, Application US/09759359A
Patent No. 6492153
GENERAL INFORMATION:
APPLICANT: ABU-THREIDH, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEROP
FILE REFERENCE: CLO01043
CURRENT APPLICATION NUMBER: US/09/759,359A
CURRENT FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 90541
TYPE: DNA
ORGANISM: Human
US-09-759-359A-3

Query Match 2.7%; Score 17; DB 4; Length 90541;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 TGTAAGTTGTGCAT 337
|||||
DB 19972 TGTAAGTTGTGCAT 19988

RESULT 35
US-09-798-096-10/c
Sequence 10, Application US/09798096
Patent No. 6393578
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECD2 EXPRESSION
FILE REFERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-798-096-10

Query Match 2.7%; Score 17; DB 4; Length 99500;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 278 CAATATTACTTTTATT 294
Db 18670 CAATATTACTTTTATT 18654

RESULT 36
US-09-585-858-1/c
Sequence 1, Application US/09585858

Patent No. 6492161
GENERAL INFORMATION:
APPLICANT: Sigridur Hjorleifsdottir
APPLICANT: Gudmundur O. Hreigvansson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Arnthor Avarsson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
FILE REFERENCE: 2739.1001-001
CURRENT APPLICATION NUMBER: US/09/585,858
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/137,120
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 129908
TYPE: DNA
ORGANISM: Bacteriophage RM378
US-09-585-858-1

Query Match 2.7%; Score 17; DB 4; Length 129908;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 423 ACTGTTCGACTTTTAC 439
Db 32762 ACTGTTCGACTTTTAC 32746

RESULT 37
US-09-557-884-1

Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match 2.7%; Score 17; DB 4; Length 1830121;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 234 TTATTATTATTATGTTG 250
Db 466814 TTATTATTATTATGTTG 466830

RESULT 38
US-09-643-990A-1

Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
Hamilton O. Smith

TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match 2.7%; Score 17; DB 4; Length 1830121;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 TTTATTATTATTATGTTG 250
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DB 466814 TTTATTATTATTATGTTG 466830

RESULT 39
US-08-290-937B-7/c
Sequence 7, Application US/08290937B
Patent No. 5648233
GENERAL INFORMATION:
APPLICANT: YAMAGUCHI, KYOJI
APPLICANT: SHIMA, NOBUYUKI
APPLICANT: MURAKAMI, AKIHIKO
APPLICANT: GOTO, MASAAKI
APPLICANT: TSUDA, EISUKE
APPLICANT: MASUNAGA, HIROAKI
APPLICANT: TAKAHIRA, REIKO
APPLICANT: OOGAKI, FUMIKO
APPLICANT: UEDA, MASATOSUGU
APPLICANT: HIGASHIO, KANUJI
TITLE OF INVENTION: MODIFIED TCF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tesla, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,937B
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-022
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OLIGONUCLEOTIDE"
US-08-290-937B-7

Query Match 2.6%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTCTGATGATCCCG 17
|||||
DB 17 TGTCTGATGATCCCG 2

RESULT 40
US-08-552-369-3/c

Sequence 3, Application US/08552369
Patent No. 6241989

GENERAL INFORMATION:
APPLICANT: Scott, Fred W.
APPLICANT: Ngichabe, Christopher K.
APPLICANT: Hu, Liangbiao
TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One Mt Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Kb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/552,369
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/190,789
FILING DATE: 01/27/1994
APPLICATION NUMBER: 07/726,609
FILING DATE: 07/09/1991
ATTORNEY/AGENT INFORMATION:

NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 18617.0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 44 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOHETICAL: no
FEATURE: P11 late promoter and leader sequence
US-08-552-369-3

Query Match 2.6%; Score 16; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTCTACTATATTTT 190
|||||
DB 16 TTCTACTATATTTT 1

Search completed: October 8, 2003, 07:53:20
Job time : 92 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 07:19:17 ; Search time 190 Seconds

(without alignments)
8494.593 Million cell updates/sec

Title: US-10-010-160-1

Perfect score: 622

Sequence: 1 atgtcgtatgcaccagtaa.....aattatgcagtcgcagatc 622

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1731049 seqs, 1297405648 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Published Applications NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCR_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|--------------------|
| 1 | 622 | 100.0 | 622 | US-10-010-160-1 | Sequence 1, Appl1 |
| 2 | 20 | 3.2 | 622 | US-10-027-632-47579 | Sequence 47579, A |
| 3 | 20 | 3.2 | 624 | US-10-027-632-75231 | Sequence 75231, A |
| 4 | 20 | 3.2 | 624 | US-10-027-632-313525 | Sequence 313525, A |
| 5 | 19 | 3.1 | 340 | US-10-060-036-1428 | Sequence 1428, Ap |
| 6 | 19 | 3.1 | 390 | US-09-864-761-5935 | Sequence 5935, Ap |
| 7 | 19 | 3.1 | 636 | US-10-027-632-220095 | Sequence 220095, A |
| 8 | 19 | 3.1 | 636 | US-10-027-632-220096 | Sequence 220096, A |
| 9 | 19 | 3.1 | 636 | US-10-027-632-220097 | Sequence 220097, A |
| 10 | 19 | 3.1 | 636 | US-10-027-632-220098 | Sequence 220098, A |
| 11 | 19 | 3.1 | 636 | US-10-027-632-220099 | Sequence 220099, A |
| 12 | 19 | 3.1 | 636 | US-10-027-632-220100 | Sequence 220100, A |
| 13 | 19 | 3.1 | 948 | US-10-313-542-28 | Sequence 28, Appl1 |
| 14 | 19 | 3.1 | 989 | US-09-887-527-53 | Sequence 53, Appl1 |
| 15 | 19 | 3.1 | 2422 | US-09-764-891-8977 | Sequence 8977, Ap |
| 16 | 19 | 3.1 | 2422 | US-09-764-891-8978 | Sequence 8978, Ap |

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| 17 | 19 | 3.1 | 3318 | US-10-044-090-452 | Sequence 452, App |
| 18 | 19 | 3.1 | 10468 | US-09-764-891-8976 | Sequence 8976, Ap |
| 19 | 19 | 3.1 | 10468 | US-09-764-891-8979 | Sequence 8979, Ap |
| 20 | 19 | 3.1 | 42500 | US-10-007-078-10 | Sequence 10, Appl1 |
| 21 | 19 | 3.1 | 161280 | US-10-144-649A-746 | Sequence 746, App |
| 22 | 19 | 3.1 | 513509 | US-09-754-853A-4 | Sequence 4, Appl1 |
| 23 | 19 | 3.1 | 1503841 | US-09-795-668-1 | Sequence 1, Appl1 |
| 24 | 19 | 3.1 | 1503841 | US-09-795-668-1 | Sequence 1, Appl1 |
| 25 | 19 | 3.1 | 1503841 | US-09-946-807-1 | Sequence 1, Appl1 |
| 26 | 19 | 3.1 | 1503841 | US-10-067-514-1 | Sequence 1, Appl1 |
| 27 | 19 | 3.1 | 1386778 | US-10-027-632-174961 | Sequence 174961, A |
| 28 | 19 | 3.1 | 3309400 | US-09-738-626-1 | Sequence 1, Appl1 |
| 29 | 19 | 3.1 | 3673778 | US-10-312-841-1 | Sequence 1, Appl1 |
| 30 | 18 | 2.9 | 393 | US-09-878-574-67 | Sequence 67, Appl1 |
| 31 | 18 | 2.9 | 399 | US-10-027-632-134481 | Sequence 134481, A |
| 32 | 18 | 2.9 | 494 | US-10-027-632-192884 | Sequence 192884, A |
| 33 | 18 | 2.9 | 546 | US-09-728-445-491 | Sequence 491, App |
| 34 | 18 | 2.9 | 561 | US-09-864-761-14909 | Sequence 14909, A |
| 35 | 18 | 2.9 | 585 | US-10-027-632-215080 | Sequence 215080, A |
| 36 | 18 | 2.9 | 585 | US-10-027-632-215081 | Sequence 215081, A |
| 37 | 18 | 2.9 | 624 | US-10-027-632-192200 | Sequence 192200, A |
| 38 | 18 | 2.9 | 1114 | US-10-027-632-117860 | Sequence 117860, A |
| 39 | 18 | 2.9 | 1440 | US-09-764-870-30 | Sequence 30, Appl1 |
| 40 | 18 | 2.9 | 1440 | US-10-125-540-30 | Sequence 30, Appl1 |
| 41 | 18 | 2.9 | 2628 | US-10-241-596-127 | Sequence 127, App |
| 42 | 18 | 2.9 | 2631 | US-10-241-596-125 | Sequence 125, App |
| 43 | 18 | 2.9 | 2631 | US-10-241-596-129 | Sequence 129, App |
| 44 | 18 | 2.9 | 2643 | US-10-241-596-123 | Sequence 123, App |
| 45 | 18 | 2.9 | 2708 | US-10-241-596-131 | Sequence 131, App |
| 46 | 18 | 2.9 | 2739 | US-10-241-596-115 | Sequence 115, App |
| 47 | 18 | 2.9 | 3181 | US-10-241-596-133 | Sequence 133, App |
| 48 | 18 | 2.9 | 3819 | US-09-838-529-1 | Sequence 1, Appl1 |
| 49 | 18 | 2.9 | 3281 | US-10-198-846-12634 | Sequence 12634, A |
| 50 | 18 | 2.9 | 3647 | US-10-241-596-134 | Sequence 134, App |
| 51 | 18 | 2.9 | 3876 | US-10-051-952-4 | Sequence 4, Appl1 |
| 52 | 18 | 2.9 | 4231 | US-09-930-213-287 | Sequence 287, App |
| 53 | 18 | 2.9 | 4886 | US-10-241-596-136 | Sequence 136, App |
| 54 | 18 | 2.9 | 5076 | US-10-241-596-135 | Sequence 135, App |
| 55 | 18 | 2.9 | 5870 | US-10-205-823-1 | Sequence 1, Appl1 |
| 56 | 18 | 2.9 | 6082 | US-09-759-143-335 | Sequence 535, App |
| 57 | 18 | 2.9 | 6082 | US-09-780-669-535 | Sequence 535, App |
| 58 | 18 | 2.9 | 6082 | US-09-822-827-535 | Sequence 535, App |
| 59 | 18 | 2.9 | 6082 | US-09-895-793-535 | Sequence 535, App |
| 60 | 18 | 2.9 | 6082 | US-09-895-814-535 | Sequence 535, App |
| 61 | 18 | 2.9 | 6082 | US-10-144-678A-535 | Sequence 535, App |
| 62 | 18 | 2.9 | 6082 | US-10-294-025-535 | Sequence 535, App |
| 63 | 18 | 2.9 | 6082 | US-10-012-896-535 | Sequence 535, App |
| 64 | 18 | 2.9 | 6082 | US-10-010-940-535 | Sequence 535, App |
| 65 | 18 | 2.9 | 8102 | US-09-070-927A-244 | Sequence 244, App |
| 66 | 18 | 2.9 | 8108 | US-10-200-562-77 | Sequence 77, Appl1 |
| 67 | 18 | 2.9 | 8108 | US-10-237-551-77 | Sequence 77, Appl1 |
| 68 | 18 | 2.9 | 8108 | US-10-121-988-77 | Sequence 77, Appl1 |
| 69 | 18 | 2.9 | 8333 | US-10-311-453-1475 | Sequence 1475, App |
| 70 | 18 | 2.9 | 8333 | US-10-240-453-129 | Sequence 129, App |
| 71 | 18 | 2.9 | 8333 | US-10-239-676-113 | Sequence 113, App |
| 72 | 18 | 2.9 | 17538 | US-10-311-455-1130 | Sequence 1130, App |
| 73 | 18 | 2.9 | 51552 | US-09-733-294A-30 | Sequence 30, Appl1 |
| 74 | 18 | 2.9 | 640681 | US-09-790-988-1 | Sequence 1, Appl1 |
| 75 | 18 | 2.9 | 3673778 | US-10-312-841-1 | Sequence 1, Appl1 |
| 76 | 18 | 2.9 | 3673778 | US-10-312-841-2 | Sequence 2, Appl1 |
| 77 | 17 | 2.7 | 226 | US-09-874-138-7 | Sequence 7, Appl1 |
| 78 | 17 | 2.7 | 226 | US-10-005-842-7 | Sequence 7, Appl1 |
| 79 | 17 | 2.7 | 307 | US-09-783-590-6377 | Sequence 6327, App |
| 80 | 17 | 2.7 | 350 | US-10-198-846-13101 | Sequence 13101, A |
| 81 | 17 | 2.7 | 455 | US-10-027-632-201659 | Sequence 201659, A |
| 82 | 17 | 2.7 | 455 | US-10-027-632-201660 | Sequence 201660, A |
| 83 | 17 | 2.7 | 474 | US-09-918-995-23154 | Sequence 23154, A |
| 84 | 17 | 2.7 | 486 | US-10-027-632-194989 | Sequence 194989, A |
| 85 | 17 | 2.7 | 486 | US-10-027-632-194990 | Sequence 194990, A |
| 86 | 17 | 2.7 | 510 | US-10-027-632-61864 | Sequence 61864, A |
| 87 | 17 | 2.7 | 510 | US-10-027-632-61865 | Sequence 61865, A |
| 88 | 17 | 2.7 | 517 | US-10-027-632-215995 | Sequence 215995, A |
| 89 | 17 | 2.7 | 524 | US-10-027-632-35352 | Sequence 35352, A |

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|-------|----|-----|---------|----|-----------------------|--------------------|
| C 90 | 17 | 2.7 | 524 | 13 | US-10-027-632-35353 | Sequence 35353, A |
| C 91 | 17 | 2.7 | 528 | 10 | US-09-998-598-1146 | Sequence 1146, App |
| C 92 | 17 | 2.7 | 528 | 12 | US-09-814-353-962 | Sequence 962, App |
| C 93 | 17 | 2.7 | 528 | 12 | US-09-814-353-7331 | Sequence 7331, App |
| C 94 | 17 | 2.7 | 536 | 12 | US-09-814-353-13716 | Sequence 13716, A |
| C 95 | 17 | 2.7 | 538 | 13 | US-10-027-632-274009 | Sequence 274009, A |
| C 96 | 17 | 2.7 | 538 | 13 | US-10-027-632-274010 | Sequence 274010, A |
| C 97 | 17 | 2.7 | 538 | 13 | US-10-027-632-274011 | Sequence 274011, A |
| C 98 | 17 | 2.7 | 555 | 13 | US-10-027-632-27208 | Sequence 27208, A |
| C 99 | 17 | 2.7 | 572 | 13 | US-10-027-632-23049 | Sequence 23049, A |
| C 100 | 17 | 2.7 | 586 | 13 | US-10-027-632-191824 | Sequence 191824, A |
| C 101 | 17 | 2.7 | 586 | 13 | US-10-027-632-191825 | Sequence 191825, A |
| C 102 | 17 | 2.7 | 611 | 13 | US-10-027-632-224564 | Sequence 224564, A |
| C 103 | 17 | 2.7 | 624 | 13 | US-10-027-632-224841 | Sequence 224841, A |
| C 104 | 17 | 2.7 | 632 | 13 | US-10-027-632-191351 | Sequence 191351, A |
| C 105 | 17 | 2.7 | 637 | 13 | US-10-027-632-202228 | Sequence 202228, A |
| C 106 | 17 | 2.7 | 652 | 13 | US-10-027-632-277415 | Sequence 277415, A |
| C 107 | 17 | 2.7 | 668 | 12 | US-10-002-631C-255 | Sequence 255, App |
| C 108 | 17 | 2.7 | 701 | 13 | US-10-027-632-33553 | Sequence 33553, A |
| C 109 | 17 | 2.7 | 726 | 13 | US-10-027-632-255325 | Sequence 255325, A |
| C 110 | 17 | 2.7 | 750 | 12 | US-10-032-585-6495 | Sequence 6495, App |
| C 111 | 17 | 2.7 | 831 | 13 | US-10-027-632-10763 | Sequence 10763, A |
| C 112 | 17 | 2.7 | 840 | 13 | US-10-027-632-170366 | Sequence 170366, A |
| C 113 | 17 | 2.7 | 854 | 14 | US-10-198-846-10645 | Sequence 10645, A |
| C 114 | 17 | 2.7 | 923 | 13 | US-10-027-632-169506 | Sequence 169506, A |
| C 115 | 17 | 2.7 | 923 | 13 | US-10-027-632-169507 | Sequence 169507, A |
| C 116 | 17 | 2.7 | 1044 | 13 | US-10-027-632-117702 | Sequence 117702, A |
| C 117 | 17 | 2.7 | 1248 | 10 | US-09-938-842A-298 | Sequence 298, App |
| C 118 | 17 | 2.7 | 1337 | 13 | US-10-044-642-2 | Sequence 2, App1 |
| C 119 | 17 | 2.7 | 1351 | 13 | US-10-027-632-258839 | Sequence 258839, A |
| C 120 | 17 | 2.7 | 1799 | 9 | US-09-828-739-1 | Sequence 1, App1 |
| C 121 | 17 | 2.7 | 1799 | 10 | US-09-887-879-10 | Sequence 10, App1 |
| C 122 | 17 | 2.7 | 1799 | 10 | US-09-992-964-10 | Sequence 10, App1 |
| C 123 | 17 | 2.7 | 1799 | 12 | US-10-242-383-10 | Sequence 10, App1 |
| C 124 | 17 | 2.7 | 1799 | 12 | US-10-288-917-2 | Sequence 2, App1 |
| C 125 | 17 | 2.7 | 1799 | 13 | US-10-052-798-2 | Sequence 2, App1 |
| C 126 | 17 | 2.7 | 1799 | 14 | US-10-207-655-193 | Sequence 193, App |
| C 127 | 17 | 2.7 | 1819 | 14 | US-10-114-170-188 | Sequence 188, App |
| C 128 | 17 | 2.7 | 1864 | 13 | US-10-139-876-3 | Sequence 3, App1 |
| C 129 | 17 | 2.7 | 1864 | 13 | US-10-139-876-17 | Sequence 17, App1 |
| C 130 | 17 | 2.7 | 1864 | 13 | US-10-139-876-19 | Sequence 19, App1 |
| C 131 | 17 | 2.7 | 2000 | 10 | US-09-938-842A-4063 | Sequence 4063, App |
| C 132 | 17 | 2.7 | 2004 | 10 | US-09-887-576-223 | Sequence 223, App |
| C 133 | 17 | 2.7 | 2029 | 10 | US-09-956-095-1 | Sequence 1, App1 |
| C 134 | 17 | 2.7 | 2029 | 10 | US-09-219-345A-10 | Sequence 10, App1 |
| C 135 | 17 | 2.7 | 2029 | 10 | US-09-795-006A-118 | Sequence 118, App |
| C 136 | 17 | 2.7 | 2029 | 11 | US-09-375-248-5 | Sequence 5, App1 |
| C 137 | 17 | 2.7 | 2029 | 14 | US-10-262-538-25 | Sequence 25, App1 |
| C 138 | 17 | 2.7 | 2029 | 14 | US-10-274-953-4 | Sequence 4, App1 |
| C 139 | 17 | 2.7 | 2029 | 14 | US-10-161-694-4 | Sequence 4, App1 |
| C 140 | 17 | 2.7 | 2070 | 13 | US-10-027-632-261195 | Sequence 261195, A |
| C 141 | 17 | 2.7 | 2888 | 13 | US-10-027-632-111927 | Sequence 111927, A |
| C 142 | 17 | 2.7 | 3007 | 12 | US-10-240-453-320 | Sequence 320, App |
| C 143 | 17 | 2.7 | 3007 | 14 | US-10-239-676-220 | Sequence 220, App |
| C 144 | 17 | 2.7 | 3881 | 8 | US-08-916-625B-1 | Sequence 1, App1 |
| C 145 | 17 | 2.7 | 3964 | 9 | US-09-757-421-3 | Sequence 3, App1 |
| C 146 | 17 | 2.7 | 3964 | 10 | US-09-811-088-5 | Sequence 5, App1 |
| C 147 | 17 | 2.7 | 3964 | 14 | US-10-314-410-5 | Sequence 5, App1 |
| C 148 | 17 | 2.7 | 3975 | 12 | US-09-814-353-20256 | Sequence 20256, A |
| C 149 | 17 | 2.7 | 4051 | 9 | US-09-757-421-1 | Sequence 1, App1 |
| C 150 | 17 | 2.7 | 4051 | 10 | US-09-811-088-3 | Sequence 3, App1 |
| C 151 | 17 | 2.7 | 4051 | 14 | US-10-314-410-3 | Sequence 3, App1 |
| C 152 | 17 | 2.7 | 4053 | 14 | US-10-037-270-156 | Sequence 156, App |
| C 153 | 17 | 2.7 | 4168 | 13 | US-10-042-417-27 | Sequence 27, App1 |
| C 154 | 17 | 2.7 | 5040 | 12 | US-10-311-455-2378 | Sequence 2378, App |
| C 155 | 17 | 2.7 | 5144 | 9 | US-09-824-735-1 | Sequence 1, App1 |
| C 156 | 17 | 2.7 | 5396 | 12 | US-10-240-485-153 | Sequence 153, App |
| C 157 | 17 | 2.7 | 5397 | 12 | US-10-311-455-1017 | Sequence 1017, App |
| C 158 | 17 | 2.7 | 5929 | 12 | US-10-311-455-682 | Sequence 682, App |
| C 159 | 17 | 2.7 | 5930 | 12 | US-09-814-353-19600 | Sequence 19600, A |
| C 160 | 17 | 2.7 | 6113 | 12 | US-10-311-455-775 | Sequence 775, App1 |
| C 161 | 17 | 2.7 | 6227 | 12 | US-10-240-485-52 | Sequence 52, App1 |
| C 162 | 17 | 2.7 | 6531 | 12 | US-10-311-455-613 | Sequence 613, App |
| C 163 | 17 | 2.7 | 6853 | 12 | US-10-311-455-284 | Sequence 284, App |
| C 164 | 17 | 2.7 | 6853 | 12 | US-10-240-452-32 | Sequence 32, App1 |
| C 165 | 17 | 2.7 | 7529 | 12 | US-10-311-455-2131 | Sequence 2131, App |
| C 166 | 17 | 2.7 | 7573 | 10 | US-09-880-107-2195 | Sequence 2195, App |
| C 167 | 17 | 2.7 | 7634 | 10 | US-10-198-846-10420 | Sequence 10420, A |
| C 168 | 17 | 2.7 | 9110 | 12 | US-10-311-455-2402 | Sequence 2402, App |
| C 169 | 17 | 2.7 | 12211 | 12 | US-10-311-455-627 | Sequence 627, App |
| C 170 | 17 | 2.7 | 59446 | 12 | US-09-820-449-3 | Sequence 3, App1 |
| C 171 | 17 | 2.7 | 90541 | 9 | US-09-759-359A-3 | Sequence 3, App1 |
| C 172 | 17 | 2.7 | 90541 | 12 | US-10-207-273-3 | Sequence 3, App1 |
| C 173 | 17 | 2.7 | 107820 | 12 | US-09-792-616-1 | Sequence 1, App1 |
| C 174 | 17 | 2.7 | 123192 | 14 | US-10-175-523-71 | Sequence 71, App1 |
| C 175 | 17 | 2.7 | 123908 | 14 | US-10-270-875-1 | Sequence 1, App1 |
| C 176 | 17 | 2.7 | 123908 | 14 | US-10-270-878-1 | Sequence 1, App1 |
| C 177 | 17 | 2.7 | 123908 | 14 | US-10-270-878-1 | Sequence 1, App1 |
| C 178 | 17 | 2.7 | 123908 | 14 | US-10-270-878-1 | Sequence 1, App1 |
| C 179 | 17 | 2.7 | 123908 | 14 | US-10-270-859-1 | Sequence 1, App1 |
| C 180 | 17 | 2.7 | 123908 | 15 | US-10-270-846-1 | Sequence 1, App1 |
| C 181 | 17 | 2.7 | 159095 | 14 | US-10-017-128-3 | Sequence 3, App1 |
| C 182 | 17 | 2.7 | 378361 | 11 | US-09-901-136-3 | Sequence 3, App1 |
| C 183 | 17 | 2.7 | 659158 | 10 | US-09-771-208-20 | Sequence 20, App1 |
| C 184 | 17 | 2.7 | 1681139 | 14 | US-10-067-514-1 | Sequence 1, App1 |
| C 185 | 17 | 2.7 | 1830121 | 14 | US-10-329-960-1 | Sequence 1, App1 |
| C 186 | 17 | 2.7 | 3309400 | 10 | US-09-738-626-1 | Sequence 1, App1 |
| C 187 | 17 | 2.7 | 9025608 | 14 | US-10-156-761-1 | Sequence 1, App1 |
| C 188 | 17 | 2.6 | 65 | 12 | US-09-832-899-15 | Sequence 15, App1 |
| C 189 | 17 | 2.6 | 65 | 12 | US-09-908-875-25530 | Sequence 2530, App |
| C 190 | 17 | 2.6 | 111 | 12 | US-09-832-899-13 | Sequence 13, App1 |
| C 191 | 17 | 2.6 | 140 | 9 | US-09-864-761-30072 | Sequence 30072, A |
| C 192 | 17 | 2.6 | 155 | 14 | US-10-102-806-417 | Sequence 417, App |
| C 193 | 17 | 2.6 | 173 | 10 | US-09-783-590-3094 | Sequence 3094, App |
| C 194 | 17 | 2.6 | 235 | 9 | US-09-923-876-6-115 | Sequence 315, App |
| C 195 | 17 | 2.6 | 258 | 10 | US-09-878-574-7240 | Sequence 7240, App |
| C 196 | 17 | 2.6 | 261 | 14 | US-10-083-357-508 | Sequence 508, App |
| C 197 | 17 | 2.6 | 268 | 9 | US-09-923-876-977 | Sequence 977, App |
| C 198 | 17 | 2.6 | 269 | 9 | US-09-764-860-88 | Sequence 88, App1 |
| C 199 | 17 | 2.6 | 269 | 14 | US-10-074-095-88 | Sequence 88, App1 |
| C 200 | 17 | 2.6 | 270 | 14 | US-10-083-357-91 | Sequence 91, App1 |
| C 201 | 17 | 2.6 | 286 | 10 | US-09-878-574-8266 | Sequence 8266, App |
| C 202 | 17 | 2.6 | 292 | 10 | US-09-867-701-6904 | Sequence 6904, App |
| C 203 | 17 | 2.6 | 307 | 14 | US-10-178-213-295 | Sequence 295, App |
| C 204 | 17 | 2.6 | 314 | 9 | US-09-775-938A-23 | Sequence 23, App1 |
| C 205 | 17 | 2.6 | 315 | 9 | US-09-775-938A-9 | Sequence 9, App1 |
| C 206 | 17 | 2.6 | 350 | 10 | US-09-783-590-1609 | Sequence 1609, App |
| C 207 | 17 | 2.6 | 352 | 9 | US-09-728-446-131 | Sequence 31, App |
| C 208 | 17 | 2.6 | 391 | 10 | US-09-981-453-154 | Sequence 154, App |
| C 209 | 17 | 2.6 | 391 | 14 | US-10-158-646-25 | Sequence 25, App1 |
| C 210 | 17 | 2.6 | 396 | 9 | US-09-864-761-22385 | Sequence 22385, A |
| C 211 | 17 | 2.6 | 404 | 11 | US-09-918-995-33593 | Sequence 33593, A |
| C 212 | 17 | 2.6 | 405 | 11 | US-09-918-995-33569 | Sequence 33569, A |
| C 213 | 17 | 2.6 | 410 | 10 | US-09-983-965-4017 | Sequence 4017, App |
| C 214 | 17 | 2.6 | 413 | 13 | US-10-027-632-39626 | Sequence 39626, A |
| C 215 | 17 | 2.6 | 413 | 13 | US-10-027-632-60627 | Sequence 60627, A |
| C 216 | 17 | 2.6 | 419 | 11 | US-09-918-995-4441 | Sequence 4441, App |
| C 217 | 17 | 2.6 | 419 | 11 | US-09-918-995-10781 | Sequence 10781, A |
| C 218 | 17 | 2.6 | 421 | 13 | US-10-027-632-104573 | Sequence 104573, A |
| C 219 | 17 | 2.6 | 425 | 13 | US-10-027-632-1296841 | Sequence 296841, A |
| C 220 | 17 | 2.6 | 425 | 13 | US-10-027-632-1606 | Sequence 1606, App |
| C 221 | 17 | 2.6 | 430 | 10 | US-09-983-965-4052 | Sequence 4052, App |
| C 222 | 17 | 2.6 | 441 | 10 | US-09-983-965-3969 | Sequence 3969, App |
| C 223 | 17 | 2.6 | 452 | 13 | US-10-027-632-91248 | Sequence 91248, A |
| C 224 | 17 | 2.6 | 452 | 13 | US-10-027-632-91249 | Sequence 91249, A |
| C 225 | 17 | 2.6 | 452 | 13 | US-10-027-632-91250 | Sequence 91250, A |
| C 226 | 17 | 2.6 | 452 | 13 | US-10-027-632-91251 | Sequence 91251, A |
| C 227 | 17 | 2.6 | 452 | 13 | US-10-027-632-236056 | Sequence 236056, A |
| C 228 | 17 | 2.6 | 452 | 13 | US-10-027-632-317657 | Sequence 317657, A |
| C 229 | 17 | 2.6 | 452 | 13 | US-10-027-632-317657 | Sequence 317657, A |
| C 230 | 17 | 2.6 | 452 | 13 | US-10-027-632-317657 | Sequence 317657, A |
| C 231 | 17 | 2.6 | 452 | 13 | US-10-027-632-317659 | Sequence 317659, A |
| C 232 | 17 | 2.6 | 456 | 13 | US-10-027-632-11145 | Sequence 11145, A |
| C 233 | 17 | 2.6 | 457 | 9 | US-09-735-705-306 | Sequence 306, App |
| C 234 | 17 | 2.6 | 457 | 10 | US-09-850-716A-306 | Sequence 306, App |
| C 235 | 17 | 2.6 | 457 | 10 | US-09-897-778-306 | Sequence 306, App |

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|-------|----|-----|-----|----|----------------------|----------------------|-------|----|-----|-----|----|----------------------|--------------------|
| C 236 | 16 | 2.6 | 457 | 11 | US-09-918-995-23725 | Sequence 23725, A | C 309 | 16 | 2.6 | 572 | 13 | US-10-027-632-236788 | Sequence 236788, |
| C 237 | 16 | 2.6 | 457 | 12 | US-10-117-982-306 | Sequence 306, App | C 310 | 16 | 2.6 | 572 | 13 | US-10-027-632-236789 | Sequence 236789, |
| C 238 | 16 | 2.6 | 457 | 13 | US-10-027-632-59016 | Sequence 59016, A | C 311 | 16 | 2.6 | 572 | 13 | US-10-027-632-236790 | Sequence 236790, |
| C 239 | 16 | 2.6 | 459 | 13 | US-10-027-632-183056 | Sequence 183056, A | C 312 | 16 | 2.6 | 575 | 13 | US-10-027-632-78488 | Sequence 78488, A |
| C 240 | 16 | 2.6 | 459 | 13 | US-10-027-632-183057 | Sequence 183057, A | C 313 | 16 | 2.6 | 575 | 13 | US-10-027-632-78489 | Sequence 78489, A |
| C 241 | 16 | 2.6 | 467 | 13 | US-10-027-632-43904 | Sequence 43904, A | C 314 | 16 | 2.6 | 575 | 13 | US-10-027-632-78975 | Sequence 78975, A |
| C 242 | 16 | 2.6 | 467 | 13 | US-10-027-632-43905 | Sequence 43905, A | C 315 | 16 | 2.6 | 575 | 13 | US-10-027-632-78976 | Sequence 78976, A |
| C 243 | 16 | 2.6 | 470 | 9 | US-09-864-761-1460 | Sequence 1460, App | C 316 | 16 | 2.6 | 575 | 13 | US-10-027-632-300824 | Sequence 300824, |
| C 244 | 16 | 2.6 | 471 | 11 | US-09-918-995-21299 | Sequence 21299, A | C 317 | 16 | 2.6 | 577 | 13 | US-10-027-632-300825 | Sequence 300825, |
| C 245 | 16 | 2.6 | 474 | 11 | US-09-918-995-22891 | Sequence 22891, A | C 318 | 16 | 2.6 | 577 | 13 | US-10-027-632-249565 | Sequence 249565, |
| C 246 | 16 | 2.6 | 481 | 13 | US-10-027-632-275760 | Sequence 275760, A | C 319 | 16 | 2.6 | 577 | 13 | US-10-027-632-249566 | Sequence 249566, |
| C 247 | 16 | 2.6 | 482 | 10 | US-09-917-800A-581 | Sequence 581, App | C 320 | 16 | 2.6 | 577 | 13 | US-10-027-632-249566 | Sequence 249566, |
| C 248 | 16 | 2.6 | 482 | 11 | US-09-918-995-16005 | Sequence 16005, A | C 321 | 16 | 2.6 | 578 | 9 | US-09-864-761-9937 | Sequence 9937, App |
| C 249 | 16 | 2.6 | 488 | 9 | US-09-864-761-11641 | Sequence 11641, A | C 322 | 16 | 2.6 | 583 | 9 | US-09-864-761-13527 | Sequence 13527, A |
| C 250 | 16 | 2.6 | 490 | 13 | US-10-027-632-185355 | Sequence 185355, A | C 323 | 16 | 2.6 | 585 | 13 | US-10-027-632-205656 | Sequence 205656, |
| C 251 | 16 | 2.6 | 491 | 13 | US-10-027-632-6415 | Sequence 6415, App | C 324 | 16 | 2.6 | 585 | 13 | US-10-027-632-205657 | Sequence 205657, |
| C 252 | 16 | 2.6 | 491 | 13 | US-10-027-632-6416 | Sequence 6416, App | C 325 | 16 | 2.6 | 585 | 13 | US-10-027-632-223078 | Sequence 223078, |
| C 253 | 16 | 2.6 | 491 | 13 | US-10-027-632-324635 | Sequence 324635, App | C 326 | 16 | 2.6 | 590 | 13 | US-10-027-632-213503 | Sequence 213503, |
| C 254 | 16 | 2.6 | 493 | 10 | US-09-070-927A-822 | Sequence 822, App | C 327 | 16 | 2.6 | 591 | 13 | US-10-027-632-255294 | Sequence 255294, |
| C 255 | 16 | 2.6 | 493 | 13 | US-10-027-632-274838 | Sequence 274838, App | C 328 | 16 | 2.6 | 591 | 13 | US-10-027-632-255295 | Sequence 255295, |
| C 256 | 16 | 2.6 | 496 | 9 | US-09-864-761-5616 | Sequence 5616, App | C 329 | 16 | 2.6 | 596 | 13 | US-10-027-632-84421 | Sequence 84421, A |
| C 257 | 16 | 2.6 | 503 | 12 | US-09-921-406C-30 | Sequence 30, App | C 330 | 16 | 2.6 | 596 | 13 | US-10-027-632-296831 | Sequence 296831, |
| C 258 | 16 | 2.6 | 505 | 11 | US-09-746-783-17 | Sequence 17, App | C 331 | 16 | 2.6 | 598 | 9 | US-09-864-761-6378 | Sequence 6378, App |
| C 259 | 16 | 2.6 | 506 | 13 | US-09-783-590-5680 | Sequence 5680, App | C 332 | 16 | 2.6 | 598 | 13 | US-10-027-632-218791 | Sequence 218791, |
| C 260 | 16 | 2.6 | 518 | 13 | US-10-027-632-126177 | Sequence 126177, A | C 333 | 16 | 2.6 | 598 | 13 | US-10-027-632-218792 | Sequence 218792, |
| C 261 | 16 | 2.6 | 519 | 13 | US-10-027-632-41720 | Sequence 41720, A | C 334 | 16 | 2.6 | 599 | 13 | US-10-027-632-103 | Sequence 103, App |
| C 262 | 16 | 2.6 | 520 | 13 | US-10-027-632-208269 | Sequence 208269, A | C 335 | 16 | 2.6 | 599 | 13 | US-10-027-632-104 | Sequence 104, App |
| C 263 | 16 | 2.6 | 520 | 13 | US-10-027-632-208270 | Sequence 208270, A | C 336 | 16 | 2.6 | 599 | 13 | US-10-027-632-105 | Sequence 105, App |
| C 264 | 16 | 2.6 | 525 | 10 | US-09-974-300-5987 | Sequence 5987, App | C 337 | 16 | 2.6 | 599 | 13 | US-10-027-632-60264 | Sequence 60264, A |
| C 265 | 16 | 2.6 | 530 | 13 | US-10-027-632-65517 | Sequence 65517, A | C 338 | 16 | 2.6 | 601 | 13 | US-10-027-632-262132 | Sequence 262132, |
| C 266 | 16 | 2.6 | 530 | 13 | US-10-027-632-296405 | Sequence 296405, A | C 339 | 16 | 2.6 | 601 | 13 | US-10-027-632-262133 | Sequence 262133, |
| C 267 | 16 | 2.6 | 533 | 13 | US-10-027-632-240455 | Sequence 240455, A | C 340 | 16 | 2.6 | 602 | 13 | US-10-027-632-205823 | Sequence 205823, |
| C 268 | 16 | 2.6 | 535 | 13 | US-10-027-632-206990 | Sequence 206990, A | C 341 | 16 | 2.6 | 604 | 11 | US-09-791-279-103 | Sequence 103, App |
| C 269 | 16 | 2.6 | 539 | 13 | US-10-027-632-281638 | Sequence 281638, A | C 342 | 16 | 2.6 | 604 | 13 | US-10-027-632-54421 | Sequence 54421, A |
| C 270 | 16 | 2.6 | 539 | 13 | US-10-027-632-281639 | Sequence 281639, A | C 343 | 16 | 2.6 | 604 | 13 | US-10-027-632-54422 | Sequence 54422, A |
| C 271 | 16 | 2.6 | 542 | 13 | US-10-027-632-50517 | Sequence 50517, A | C 344 | 16 | 2.6 | 604 | 13 | US-10-027-632-54423 | Sequence 54423, A |
| C 272 | 16 | 2.6 | 542 | 13 | US-10-027-632-50518 | Sequence 50518, A | C 345 | 16 | 2.6 | 604 | 13 | US-10-027-632-301577 | Sequence 301577, |
| C 273 | 16 | 2.6 | 542 | 13 | US-10-027-632-306621 | Sequence 306621, A | C 346 | 16 | 2.6 | 604 | 13 | US-10-027-632-301578 | Sequence 301578, |
| C 274 | 16 | 2.6 | 542 | 13 | US-10-027-632-306622 | Sequence 306622, A | C 347 | 16 | 2.6 | 604 | 13 | US-10-027-632-301579 | Sequence 301579, |
| C 275 | 16 | 2.6 | 543 | 13 | US-10-027-632-264798 | Sequence 264798, A | C 348 | 16 | 2.6 | 608 | 13 | US-10-027-632-216069 | Sequence 216069, |
| C 276 | 16 | 2.6 | 543 | 13 | US-10-027-632-264799 | Sequence 264799, A | C 349 | 16 | 2.6 | 611 | 13 | US-10-027-632-202649 | Sequence 202649, |
| C 277 | 16 | 2.6 | 546 | 13 | US-10-027-632-307649 | Sequence 307649, A | C 350 | 16 | 2.6 | 611 | 13 | US-10-027-632-208484 | Sequence 208484, |
| C 278 | 16 | 2.6 | 546 | 13 | US-10-027-632-32106 | Sequence 32106, A | C 351 | 16 | 2.6 | 614 | 13 | US-10-027-632-99733 | Sequence 99733, A |
| C 279 | 16 | 2.6 | 548 | 13 | US-10-027-632-82343 | Sequence 82343, A | C 352 | 16 | 2.6 | 615 | 12 | US-09-814-353-3575 | Sequence 3575, App |
| C 280 | 16 | 2.6 | 548 | 13 | US-10-027-632-82344 | Sequence 82344, A | C 353 | 16 | 2.6 | 615 | 12 | US-09-814-353-9889 | Sequence 9889, App |
| C 281 | 16 | 2.6 | 548 | 13 | US-10-027-632-83251 | Sequence 83251, A | C 354 | 16 | 2.6 | 615 | 13 | US-10-051-902-17 | Sequence 17, App |
| C 282 | 16 | 2.6 | 548 | 13 | US-10-027-632-83252 | Sequence 83252, A | C 355 | 16 | 2.6 | 615 | 13 | US-10-027-632-175152 | Sequence 175152, |
| C 283 | 16 | 2.6 | 549 | 13 | US-10-027-632-51135 | Sequence 51135, A | C 356 | 16 | 2.6 | 615 | 13 | US-10-027-632-255157 | Sequence 255157, |
| C 284 | 16 | 2.6 | 549 | 13 | US-10-027-632-51136 | Sequence 51136, A | C 357 | 16 | 2.6 | 615 | 13 | US-10-027-632-255157 | Sequence 255157, |
| C 285 | 16 | 2.6 | 555 | 13 | US-10-027-632-222300 | Sequence 222300, A | C 358 | 16 | 2.6 | 620 | 12 | US-09-814-353-16273 | Sequence 16273, A |
| C 286 | 16 | 2.6 | 555 | 13 | US-10-027-632-222300 | Sequence 222300, A | C 359 | 16 | 2.6 | 622 | 13 | US-10-027-632-272937 | Sequence 272937, |
| C 287 | 16 | 2.6 | 559 | 13 | US-10-027-632-219347 | Sequence 219347, A | C 360 | 16 | 2.6 | 622 | 13 | US-10-027-632-272938 | Sequence 272938, |
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| C 292 | 16 | 2.6 | 564 | 13 | US-10-027-632-90534 | Sequence 90534, A | C 365 | 16 | 2.6 | 632 | 13 | US-10-027-632-129060 | Sequence 129060, |
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| C 294 | 16 | 2.6 | 565 | 13 | US-10-027-632-38862 | Sequence 38862, A | C 367 | 16 | 2.6 | 633 | 13 | US-10-027-632-196659 | Sequence 196659, |
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| C 298 | 16 | 2.6 | 567 | 11 | US-09-918-995-12528 | Sequence 12528, A | C 371 | 16 | 2.6 | 641 | 13 | US-10-027-632-221632 | Sequence 221632, |
| C 299 | 16 | 2.6 | 567 | 13 | US-10-027-632-65674 | Sequence 65674, A | C 372 | 16 | 2.6 | 644 | 13 | US-10-027-632-116150 | Sequence 116150, |
| C 300 | 16 | 2.6 | 567 | 13 | US-10-027-632-65675 | Sequence 65675, A | C 373 | 16 | 2.6 | 646 | 13 | US-10-027-632-206528 | Sequence 206528, |
| C 301 | 16 | 2.6 | 567 | 13 | US-10-027-632-198285 | Sequence 198285, A | C 374 | 16 | 2.6 | 649 | 13 | US-10-027-632-46290 | Sequence 46290, A |
| C 302 | 16 | 2.6 | 567 | 13 | US-10-027-632-198286 | Sequence 198286, A | C 375 | 16 | 2.6 | 649 | 13 | US-10-027-632-46291 | Sequence 46291, A |
| C 303 | 16 | 2.6 | 567 | 13 | US-10-027-632-295865 | Sequence 295865, A | C 376 | 16 | 2.6 | 649 | 13 | US-10-027-632-228874 | Sequence 228874, |
| C 304 | 16 | 2.6 | 567 | 13 | US-10-027-632-295866 | Sequence 295866, A | C 377 | 16 | 2.6 | 650 | 13 | US-10-027-632-211107 | Sequence 211107, |
| C 305 | 16 | 2.6 | 568 | 9 | US-09-864-761-9029 | Sequence 9029, App | C 378 | 16 | 2.6 | 653 | 13 | US-10-027-632-206121 | Sequence 206121, |
| C 306 | 16 | 2.6 | 569 | 13 | US-10-027-632-270693 | Sequence 270693, App | C 379 | 16 | 2.6 | 655 | 13 | US-10-027-632-206121 | Sequence 206121, |
| C 307 | 16 | 2.6 | 571 | 13 | US-10-027-632-254618 | Sequence 254618, App | C 380 | 16 | 2.6 | 656 | 11 | US-09-764-891-8741 | Sequence 8741, App |
| C 308 | 16 | 2.6 | 572 | 11 | US-09-911-904-233 | Sequence 233, App | C 381 | 16 | 2.6 | 656 | 13 | US-10-027-632-252418 | Sequence 252418, |

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| 332 | 16 | 2.6 | 659 | 13 | US-10-027-632-111125 | Sequence 111125, | C 455 | 16 | 2.6 | 1225 | 13 | US-10-027-632-265686 | Sequence 265686, |
| C 333 | 16 | 2.6 | 660 | 13 | US-10-027-632-215139 | Sequence 215139, | C 456 | 16 | 2.6 | 1225 | 13 | US-10-027-632-265687 | Sequence 265687, |
| C 334 | 16 | 2.6 | 663 | 13 | US-10-027-632-79909 | Sequence 79909, A | C 457 | 16 | 2.6 | 1234 | 13 | US-10-027-632-122693 | Sequence 123693, |
| C 335 | 16 | 2.6 | 663 | 13 | US-10-027-632-79910 | Sequence 79910, A | C 458 | 16 | 2.6 | 1236 | 9 | US-09-918-686-19 | Sequence 19, Appl |
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| 337 | 16 | 2.6 | 663 | 13 | US-10-027-632-182690 | Sequence 182690, | C 460 | 16 | 2.6 | 1255 | 10 | US-09-764-877-3303 | Sequence 3303, Ap |
| 338 | 16 | 2.6 | 664 | 13 | US-10-027-632-283561 | Sequence 283561, | C 461 | 16 | 2.6 | 1276 | 14 | US-10-198-846-10516 | Sequence 10516, A |
| 339 | 16 | 2.6 | 667 | 13 | US-10-027-632-275833 | Sequence 275833, | C 462 | 16 | 2.6 | 1321 | 16 | US-10-027-632-123492 | Sequence 123492, |
| C 330 | 16 | 2.6 | 670 | 12 | US-10-133-013-88 | Sequence 88, Appl | C 463 | 16 | 2.6 | 1326 | 12 | US-10-255-649A-2 | Sequence 2, Appl1 |
| C 331 | 16 | 2.6 | 676 | 13 | US-10-027-632-18926 | Sequence 18926, A | C 464 | 16 | 2.6 | 1344 | 14 | US-10-081-309-1 | Sequence 1, Appl1 |
| C 332 | 16 | 2.6 | 698 | 13 | US-10-027-632-280732 | Sequence 280732, | C 465 | 16 | 2.6 | 1346 | 13 | US-10-027-632-122761 | Sequence 122761, |
| C 333 | 16 | 2.6 | 708 | 13 | US-10-027-632-257980 | Sequence 257980, A | C 466 | 16 | 2.6 | 1346 | 13 | US-10-027-632-122762 | Sequence 122762, |
| C 334 | 16 | 2.6 | 709 | 13 | US-10-027-632-249390 | Sequence 249390, | C 467 | 16 | 2.6 | 1382 | 10 | US-09-764-847-1253 | Sequence 1253, Ap |
| C 335 | 16 | 2.6 | 720 | 13 | US-10-027-632-21419 | Sequence 21419, A | C 468 | 16 | 2.6 | 1382 | 14 | US-10-092-154-1253 | Sequence 1253, Ap |
| C 336 | 16 | 2.6 | 726 | 13 | US-10-027-632-173428 | Sequence 173428, | C 469 | 16 | 2.6 | 1518 | 12 | US-10-032-585-6015 | Sequence 6015, Ap |
| C 337 | 16 | 2.6 | 729 | 13 | US-10-027-632-14417 | Sequence 14417, A | C 470 | 16 | 2.6 | 1523 | 13 | US-10-027-632-259006 | Sequence 259006, |
| 338 | 16 | 2.6 | 729 | 13 | US-10-027-632-33775 | Sequence 33775, A | C 471 | 16 | 2.6 | 1523 | 13 | US-10-044-090-141 | Sequence 141, App |
| 339 | 16 | 2.6 | 731 | 13 | US-10-027-632-33776 | Sequence 33776, A | C 472 | 16 | 2.6 | 1556 | 13 | US-10-044-090-140 | Sequence 140, App |
| 400 | 16 | 2.6 | 731 | 13 | US-10-027-632-33777 | Sequence 33777, A | C 473 | 16 | 2.6 | 1575 | 9 | US-09-815-242-6845 | Sequence 6845, Ap |
| 401 | 16 | 2.6 | 731 | 13 | US-10-027-632-33777 | Sequence 33777, A | C 474 | 16 | 2.6 | 1581 | 13 | US-10-027-632-259402 | Sequence 259402, |
| 402 | 16 | 2.6 | 732 | 13 | US-10-027-632-285196 | Sequence 285196, | C 475 | 16 | 2.6 | 1591 | 14 | US-09-974-300-1840 | Sequence 1840, Ap |
| C 403 | 16 | 2.6 | 732 | 13 | US-10-027-632-285197 | Sequence 285197, | C 476 | 16 | 2.6 | 1641 | 10 | US-09-070-927A-582 | Sequence 582, App |
| C 404 | 16 | 2.6 | 732 | 13 | US-10-027-632-285198 | Sequence 285198, | C 477 | 16 | 2.6 | 1677 | 13 | US-10-044-090-140 | Sequence 140, App |
| C 405 | 16 | 2.6 | 733 | 13 | US-10-027-632-11575 | Sequence 11575, A | C 478 | 16 | 2.6 | 1779 | 9 | US-09-764-860-774 | Sequence 774, App |
| C 406 | 16 | 2.6 | 736 | 9 | US-09-775-938A-11 | Sequence 11, Appl | C 479 | 16 | 2.6 | 1779 | 14 | US-10-074-095-774 | Sequence 774, App |
| C 407 | 16 | 2.6 | 740 | 13 | US-10-027-632-126357 | Sequence 126357, | C 480 | 16 | 2.6 | 1780 | 13 | US-09-764-860-773 | Sequence 773, App |
| C 408 | 16 | 2.6 | 750 | 13 | US-10-027-632-282240 | Sequence 282240, | C 481 | 16 | 2.6 | 1780 | 14 | US-10-074-095-773 | Sequence 9853, A |
| C 409 | 16 | 2.6 | 758 | 13 | US-10-027-632-144073 | Sequence 144073, | C 482 | 16 | 2.6 | 1810 | 13 | US-10-027-632-99553 | Sequence 9953, A |
| C 410 | 16 | 2.6 | 778 | 14 | US-10-175-523-15 | Sequence 15, Appl | C 483 | 16 | 2.6 | 1827 | 9 | US-09-778-927A-1 | Sequence 1, Appl1 |
| C 411 | 16 | 2.6 | 780 | 13 | US-10-027-632-29003 | Sequence 29003, A | C 484 | 16 | 2.6 | 1839 | 11 | US-09-764-891-5336 | Sequence 5396, Ap |
| 412 | 16 | 2.6 | 785 | 13 | US-10-027-632-172721 | Sequence 172721, | C 485 | 16 | 2.6 | 1850 | 12 | US-09-814-353-20826 | Sequence 20826, A |
| C 413 | 16 | 2.6 | 788 | 13 | US-10-027-632-33646 | Sequence 33646, A | C 486 | 16 | 2.6 | 1871 | 13 | US-10-027-632-36084 | Sequence 36084, A |
| C 414 | 16 | 2.6 | 803 | 13 | US-10-027-632-174228 | Sequence 174228, | C 487 | 16 | 2.6 | 1871 | 13 | US-10-027-632-36085 | Sequence 36085, A |
| C 415 | 16 | 2.6 | 811 | 13 | US-10-027-632-167050 | Sequence 167050, | C 488 | 16 | 2.6 | 1871 | 13 | US-10-027-632-36086 | Sequence 36086, A |
| C 416 | 16 | 2.6 | 818 | 13 | US-10-027-632-169140 | Sequence 169140, | C 489 | 16 | 2.6 | 1871 | 13 | US-10-027-632-36087 | Sequence 36087, A |
| C 417 | 16 | 2.6 | 820 | 13 | US-10-027-632-169141 | Sequence 169141, | C 490 | 16 | 2.6 | 1884 | 10 | US-09-938-842A-1109 | Sequence 1109, Ap |
| 418 | 16 | 2.6 | 823 | 13 | US-10-027-632-140112 | Sequence 140112, | C 491 | 16 | 2.6 | 1929 | 13 | US-10-027-632-97987 | Sequence 97987, A |
| C 419 | 16 | 2.6 | 824 | 13 | US-10-027-632-148858 | Sequence 148858, | C 492 | 16 | 2.6 | 1940 | 10 | US-09-938-842A-1336 | Sequence 1336, Ap |
| 420 | 16 | 2.6 | 834 | 13 | US-10-027-632-148855 | Sequence 148855, | C 493 | 16 | 2.6 | 2000 | 10 | US-09-938-842A-14117 | Sequence 4117, Ap |
| 421 | 16 | 2.6 | 834 | 13 | US-10-027-632-148856 | Sequence 148856, | C 494 | 16 | 2.6 | 2000 | 10 | US-09-938-842A-14137 | Sequence 4533, Ap |
| 422 | 16 | 2.6 | 834 | 13 | US-10-027-632-148857 | Sequence 148857, | C 495 | 16 | 2.6 | 2000 | 10 | US-09-938-842A-14137 | Sequence 4533, Ap |
| 423 | 16 | 2.6 | 839 | 13 | US-10-027-632-168086 | Sequence 168086, | C 496 | 16 | 2.6 | 2000 | 10 | US-09-938-842A-14137 | Sequence 4533, Ap |
| 424 | 16 | 2.6 | 839 | 13 | US-10-027-632-168087 | Sequence 168087, | C 497 | 16 | 2.6 | 2000 | 10 | US-09-938-842A-14137 | Sequence 4533, Ap |
| 425 | 16 | 2.6 | 847 | 13 | US-10-027-632-168662 | Sequence 168662, | C 498 | 16 | 2.6 | 2017 | 13 | US-10-051-909-21 | Sequence 21, Appl |
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| C 427 | 16 | 2.6 | 873 | 14 | US-10-027-632-9902 | Sequence 9902, Ap | C 500 | 16 | 2.6 | 2100 | 14 | US-10-037-632-97786 | Sequence 97786, A |
| C 428 | 16 | 2.6 | 887 | 13 | US-10-027-632-50550 | Sequence 50550, A | C 501 | 16 | 2.6 | 2163 | 13 | US-10-027-632-97787 | Sequence 97787, A |
| C 429 | 16 | 2.6 | 887 | 13 | US-10-027-632-50550 | Sequence 50550, A | C 502 | 16 | 2.6 | 2163 | 13 | US-10-027-632-102156 | Sequence 102156, |
| C 430 | 16 | 2.6 | 919 | 12 | US-09-814-353-21308 | Sequence 21308, A | C 503 | 16 | 2.6 | 2163 | 13 | US-10-027-632-102157 | Sequence 102157, |
| C 431 | 16 | 2.6 | 929 | 9 | US-09-452-239-19 | Sequence 19, Appl | C 504 | 16 | 2.6 | 2163 | 13 | US-09-833-381-2033 | Sequence 2033, Ap |
| C 432 | 16 | 2.6 | 962 | 9 | US-09-452-239-23 | Sequence 23, Appl | C 505 | 16 | 2.6 | 2178 | 12 | US-10-311-776-3 | Sequence 3, Appl1 |
| C 433 | 16 | 2.6 | 965 | 13 | US-10-027-632-10084 | Sequence 120084, | C 506 | 16 | 2.6 | 2182 | 9 | US-09-778-927A-2 | Sequence 2, Appl1 |
| C 434 | 16 | 2.6 | 980 | 9 | US-09-452-239-21 | Sequence 21, Appl1 | C 507 | 16 | 2.6 | 2184 | 9 | US-09-778-927A-2 | Sequence 34, Appl |
| C 435 | 16 | 2.6 | 1010 | 13 | US-10-027-632-119331 | Sequence 119331, | C 508 | 16 | 2.6 | 2193 | 12 | US-10-311-776-1 | Sequence 16, Appl |
| C 436 | 16 | 2.6 | 1010 | 13 | US-10-027-632-122301 | Sequence 122301, | C 509 | 16 | 2.6 | 2193 | 12 | US-10-311-776-1 | Sequence 16, Appl |
| C 437 | 16 | 2.6 | 1023 | 9 | US-09-452-239-25 | Sequence 25, Appl | C 510 | 16 | 2.6 | 2193 | 12 | US-10-311-776-1 | Sequence 16, Appl |
| C 438 | 16 | 2.6 | 1026 | 14 | US-10-102-806-168 | Sequence 168, App | C 511 | 16 | 2.6 | 2199 | 8 | US-08-605-221-1 | Sequence 1, Appl1 |
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| C 440 | 16 | 2.6 | 1034 | 13 | US-10-027-632-250681 | Sequence 250681, | C 513 | 16 | 2.6 | 2268 | 13 | US-10-027-632-102919 | Sequence 102919, |
| C 441 | 16 | 2.6 | 1067 | 13 | US-10-027-632-249826 | Sequence 249826, | C 514 | 16 | 2.6 | 2306 | 13 | US-10-027-632-101671 | Sequence 101671, |
| C 442 | 16 | 2.6 | 1099 | 12 | US-10-017-161-2253 | Sequence 2253, Ap | C 515 | 16 | 2.6 | 2426 | 13 | US-10-027-632-102237 | Sequence 102237, |
| C 443 | 16 | 2.6 | 1099 | 13 | US-10-027-632-118895 | Sequence 118895, | C 516 | 16 | 2.6 | 2501 | 14 | US-10-198-846-13958 | Sequence 13958, A |
| C 444 | 16 | 2.6 | 1100 | 13 | US-10-027-632-119651 | Sequence 119652, | C 517 | 16 | 2.6 | 2530 | 10 | US-09-764-877-2332 | Sequence 2332, Ap |
| C 445 | 16 | 2.6 | 1100 | 13 | US-10-027-632-119652 | Sequence 119652, | C 518 | 16 | 2.6 | 2628 | 12 | US-10-032-585-6857 | Sequence 6857, Ap |
| C 446 | 16 | 2.6 | 1161 | 13 | US-10-027-632-118237 | Sequence 118237, | C 519 | 16 | 2.6 | 2674 | 14 | US-10-032-585-6415 | Sequence 6415, Ap |
| C 447 | 16 | 2.6 | 1161 | 13 | US-10-027-632-118237 | Sequence 118237, | C 520 | 16 | 2.6 | 2824 | 14 | US-10-025-567A-59 | Sequence 59, Appl |
| C 448 | 16 | 2.6 | 1162 | 13 | US-10-027-632-205822 | Sequence 205822, | C 521 | 16 | 2.6 | 2866 | 13 | US-10-027-632-112075 | Sequence 112075, |
| C 449 | 16 | 2.6 | 1169 | 13 | US-10-027-632-118871 | Sequence 118871, | C 522 | 16 | 2.6 | 2994 | 9 | US-09-728-628-9 | Sequence 9, Appl1 |
| C 450 | 16 | 2.6 | 1169 | 13 | US-10-027-632-118872 | Sequence 118872, | C 523 | 16 | 2.6 | 3011 | 12 | US-10-240-965-154 | Sequence 154, App |
| C 451 | 16 | 2.6 | 1169 | 13 | US-10-027-632-118873 | Sequence 118873, | C 524 | 16 | 2.6 | 3117 | 13 | US-10-027-632-114090 | Sequence 114090, |
| C 452 | 16 | 2.6 | 1178 | 13 | US-10-027-632-251821 | Sequence 251821, | C 525 | 16 | 2.6 | 3178 | 9 | US-09-729-674-165 | Sequence 165, App |
| C 453 | 16 | 2.6 | 1225 | 13 | US-10-027-632-265684 | Sequence 265684, | C 526 | 16 | 2.6 | 3178 | 9 | US-09-729-674-165 | Sequence 165, App |
| C 454 | 16 | 2.6 | 1225 | 13 | US-10-027-632-265685 | Sequence 265685, | C 527 | 16 | 2.6 | 3183 | 13 | US-10-027-632-113812 | Sequence 113812, |

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| C 528 | 16 | 2.6 | 3183 | 13 | US-10-027-632-113813 | Sequence 113813, | 601 | 16 | 2.6 | 7353 | 12 | US-10-311-455-46 | Sequence 46, Appl |
| C 529 | 16 | 2.6 | 3197 | 13 | US-10-027-632-114268 | Sequence 114268, | C 602 | 16 | 2.6 | 7403 | 12 | US-10-311-455-2189 | Sequence 2189, Ap |
| C 530 | 16 | 2.6 | 3197 | 13 | US-10-027-632-114269 | Sequence 114269, | C 603 | 16 | 2.6 | 7403 | 12 | US-10-311-455-2190 | Sequence 2190, Ap |
| C 531 | 16 | 2.6 | 3361 | 11 | US-09-764-877-2616 | Sequence 2616, Ap | C 604 | 16 | 2.6 | 7500 | 12 | US-10-311-455-1068 | Sequence 1068, Ap |
| C 532 | 16 | 2.6 | 3381 | 11 | US-09-764-891-5397 | Sequence 5397, Ap | C 605 | 16 | 2.6 | 7503 | 12 | US-10-311-455-1551 | Sequence 1551, Ap |
| C 533 | 16 | 2.6 | 3421 | 8 | US-08-781-986A-337 | Sequence 337, Ap | C 606 | 16 | 2.6 | 7676 | 12 | US-10-240-485-151 | Sequence 151, Ap |
| C 534 | 16 | 2.6 | 3495 | 11 | US-09-746-783-167 | Sequence 167, Ap | C 607 | 16 | 2.6 | 7829 | 12 | US-10-311-455-1078 | Sequence 1078, Ap |
| C 535 | 16 | 2.6 | 3599 | 12 | US-10-240-965-80 | Sequence 80, Appl | C 608 | 16 | 2.6 | 7924 | 12 | US-10-311-455-2111 | Sequence 2111, Ap |
| C 536 | 16 | 2.6 | 3731 | 14 | US-10-270-333-103 | Sequence 103, Appl | C 609 | 16 | 2.6 | 8161 | 9 | US-09-759-152-9 | Sequence 9, Appl |
| C 537 | 16 | 2.6 | 3795 | 14 | US-10-033-717-3 | Sequence 3, Appl | C 610 | 16 | 2.6 | 8166 | 12 | US-10-311-455-1765 | Sequence 1765, Ap |
| C 538 | 16 | 2.6 | 3942 | 12 | US-10-349-680-143 | Sequence 143, Appl | C 611 | 16 | 2.6 | 8175 | 12 | US-09-759-152-7 | Sequence 7, Appl |
| C 539 | 16 | 2.6 | 4020 | 11 | US-09-764-891-8742 | Sequence 8742, Ap | C 612 | 16 | 2.6 | 8406 | 12 | US-10-311-455-2418 | Sequence 2418, Ap |
| C 540 | 16 | 2.6 | 4896 | 9 | US-09-756-526A-3 | Sequence 3, Appl | C 613 | 16 | 2.6 | 9000 | 11 | US-09-949-427-3 | Sequence 3, Appl |
| C 541 | 16 | 2.6 | 4896 | 12 | US-10-345-020-3 | Sequence 3, Appl | C 614 | 16 | 2.6 | 9084 | 12 | US-10-311-455-1578 | Sequence 1578, Ap |
| C 542 | 16 | 2.6 | 4896 | 12 | US-10-342-821-3 | Sequence 3, Appl | C 615 | 16 | 2.6 | 9157 | 12 | US-10-311-455-1473 | Sequence 1473, Ap |
| C 543 | 16 | 2.6 | 5046 | 9 | US-09-725-735A-13 | Sequence 13, Appl | C 616 | 16 | 2.6 | 9206 | 12 | US-10-311-455-1647 | Sequence 1647, Ap |
| C 544 | 16 | 2.6 | 5099 | 11 | US-09-908-289-15 | Sequence 15, Appl | C 617 | 16 | 2.6 | 9876 | 12 | US-10-311-455-66 | Sequence 66, Appl |
| C 545 | 16 | 2.6 | 5099 | 14 | US-10-267-763-5 | Sequence 5, Appl | C 618 | 16 | 2.6 | 10377 | 12 | US-10-311-455-2193 | Sequence 2193, Appl |
| C 546 | 16 | 2.6 | 5110 | 13 | US-10-027-632-175153 | Sequence 175153, | C 619 | 16 | 2.6 | 11036 | 10 | US-09-908-711-166 | Sequence 166, Ap |
| C 547 | 16 | 2.6 | 5158 | 12 | US-10-326-185-108 | Sequence 108, Appl | C 620 | 16 | 2.6 | 11115 | 9 | US-09-908-711-166 | Sequence 166, Ap |
| C 548 | 16 | 2.6 | 5183 | 12 | US-10-311-455-1322 | Sequence 1322, Ap | C 621 | 16 | 2.6 | 11944 | 12 | US-10-311-455-2160 | Sequence 2160, Ap |
| C 549 | 16 | 2.6 | 5183 | 12 | US-10-240-453-312 | Sequence 312, Appl | C 622 | 16 | 2.6 | 12237 | 12 | US-10-311-455-2331 | Sequence 2331, Ap |
| C 550 | 16 | 2.6 | 5183 | 14 | US-10-239-676-214 | Sequence 214, Appl | C 623 | 16 | 2.6 | 12507 | 12 | US-10-311-455-271 | Sequence 271, Appl |
| C 551 | 16 | 2.6 | 5185 | 12 | US-10-311-455-1007 | Sequence 1007, Ap | C 624 | 16 | 2.6 | 13125 | 12 | US-10-240-452-64 | Sequence 64, Appl |
| C 552 | 16 | 2.6 | 5221 | 12 | US-10-311-455-1887 | Sequence 1887, Ap | C 625 | 16 | 2.6 | 13125 | 12 | US-10-311-455-1199 | Sequence 1199, Ap |
| C 553 | 16 | 2.6 | 5236 | 12 | US-10-311-455-323 | Sequence 323, Appl | C 626 | 16 | 2.6 | 13125 | 12 | US-10-240-485-109 | Sequence 109, Appl |
| C 554 | 16 | 2.6 | 5299 | 14 | US-10-270-333-73 | Sequence 73, Appl | C 627 | 16 | 2.6 | 13792 | 12 | US-10-311-455-1543 | Sequence 1543, Ap |
| C 555 | 16 | 2.6 | 5308 | 12 | US-10-311-455-843 | Sequence 843, Appl | C 628 | 16 | 2.6 | 14708 | 12 | US-10-311-455-2218 | Sequence 2218, Ap |
| C 556 | 16 | 2.6 | 5398 | 12 | US-10-133-013-49 | Sequence 49, Appl | C 629 | 16 | 2.6 | 14708 | 12 | US-10-240-453-324 | Sequence 324, Ap |
| C 557 | 16 | 2.6 | 5460 | 12 | US-10-311-455-1877 | Sequence 1877, Ap | C 630 | 16 | 2.6 | 17708 | 14 | US-10-239-676-222 | Sequence 222, Appl |
| C 558 | 16 | 2.6 | 5529 | 13 | US-10-027-632-175151 | Sequence 175151, | C 631 | 16 | 2.6 | 15247 | 12 | US-10-311-455-2056 | Sequence 2056, Ap |
| C 559 | 16 | 2.6 | 5729 | 12 | US-10-205-194-70 | Sequence 70, Appl | C 632 | 16 | 2.6 | 15643 | 9 | US-09-764-870-638 | Sequence 638, Appl |
| C 560 | 16 | 2.6 | 5771 | 12 | US-10-311-455-1924 | Sequence 1924, Ap | C 633 | 16 | 2.6 | 15732 | 14 | US-10-125-540-638 | Sequence 638, Appl |
| C 561 | 16 | 2.6 | 5798 | 12 | US-10-311-455-142 | Sequence 142, Appl | C 634 | 16 | 2.6 | 15732 | 12 | US-10-240-453-107 | Sequence 107, Appl |
| C 562 | 16 | 2.6 | 5844 | 12 | US-10-204-708-90 | Sequence 90, Appl | C 635 | 16 | 2.6 | 15743 | 14 | US-10-239-676-95 | Sequence 95, Appl |
| C 563 | 16 | 2.6 | 5885 | 10 | US-09-070-927A-105 | Sequence 105, Appl | C 636 | 16 | 2.6 | 15743 | 12 | US-10-240-453-270 | Sequence 270, Appl |
| C 564 | 16 | 2.6 | 5898 | 10 | US-09-880-107-7708 | Sequence 3708, Appl | C 637 | 16 | 2.6 | 16084 | 10 | US-09-764-877-2526 | Sequence 2526, Ap |
| C 565 | 16 | 2.6 | 5942 | 14 | US-10-172-086-16 | Sequence 16, Appl | C 638 | 16 | 2.6 | 17728 | 12 | US-10-311-455-1701 | Sequence 1701, Ap |
| C 566 | 16 | 2.6 | 5945 | 12 | US-10-311-455-57 | Sequence 57, Appl | C 639 | 16 | 2.6 | 17731 | 12 | US-10-311-455-1512 | Sequence 1512, Ap |
| C 567 | 16 | 2.6 | 5958 | 12 | US-10-311-455-1032 | Sequence 1032, Ap | C 640 | 16 | 2.6 | 17869 | 12 | US-10-311-455-78 | Sequence 78, Appl |
| C 568 | 16 | 2.6 | 5962 | 12 | US-10-311-455-1441 | Sequence 1441, Ap | C 641 | 16 | 2.6 | 18011 | 12 | US-10-311-455-8 | Sequence 8, Appl |
| C 569 | 16 | 2.6 | 5999 | 12 | US-10-311-455-826 | Sequence 826, Appl | C 642 | 16 | 2.6 | 19011 | 11 | US-09-764-891-5813 | Sequence 5813, Appl |
| C 570 | 16 | 2.6 | 5999 | 12 | US-10-240-453-66 | Sequence 66, Appl | C 643 | 16 | 2.6 | 19011 | 11 | US-09-764-891-5814 | Sequence 5814, Ap |
| C 571 | 16 | 2.6 | 6000 | 9 | US-09-775-938A-29 | Sequence 29, Appl | C 644 | 16 | 2.6 | 19082 | 12 | US-10-311-455-599 | Sequence 599, Appl |
| C 572 | 16 | 2.6 | 6030 | 14 | US-10-239-676-163 | Sequence 163, Appl | C 645 | 16 | 2.6 | 25002 | 12 | US-10-146-733-76 | Sequence 10041, A |
| C 573 | 16 | 2.6 | 6030 | 14 | US-10-239-676-163 | Sequence 163, Appl | C 646 | 16 | 2.6 | 25002 | 12 | US-10-024-623-31 | Sequence 31, Appl |
| C 574 | 16 | 2.6 | 6048 | 12 | US-10-311-455-2004 | Sequence 2004, Ap | C 647 | 16 | 2.6 | 25423 | 10 | US-09-764-855-193 | Sequence 193, Appl |
| C 575 | 16 | 2.6 | 6062 | 12 | US-10-311-455-2052 | Sequence 2052, Ap | C 648 | 16 | 2.6 | 25423 | 14 | US-10-072-349-193 | Sequence 193, Appl |
| C 576 | 16 | 2.6 | 6072 | 12 | US-10-311-455-3 | Sequence 3, Appl | C 649 | 16 | 2.6 | 25424 | 10 | US-09-764-855-194 | Sequence 194, Appl |
| C 577 | 16 | 2.6 | 6076 | 12 | US-10-240-453-221 | Sequence 221, Appl | C 650 | 16 | 2.6 | 25424 | 14 | US-10-072-349-194 | Sequence 194, Appl |
| C 578 | 16 | 2.6 | 6115 | 12 | US-10-311-455-1774 | Sequence 1774, Ap | C 651 | 16 | 2.6 | 25801 | 13 | US-10-193-295-3 | Sequence 3, Appl |
| C 579 | 16 | 2.6 | 6134 | 10 | US-09-764-877-3301 | Sequence 3301, Ap | C 652 | 16 | 2.6 | 28303 | 10 | US-09-764-877-3194 | Sequence 3194, Ap |
| C 580 | 16 | 2.6 | 6151 | 12 | US-10-311-455-1583 | Sequence 1583, Ap | C 653 | 16 | 2.6 | 28303 | 10 | US-09-764-877-3198 | Sequence 3198, Ap |
| C 581 | 16 | 2.6 | 6151 | 12 | US-10-240-453-149 | Sequence 149, Appl | C 654 | 16 | 2.6 | 28328 | 10 | US-10-007-010-15 | Sequence 10, Appl |
| C 582 | 16 | 2.6 | 6164 | 12 | US-10-311-455-984 | Sequence 984, Appl | C 655 | 16 | 2.6 | 30000 | 9 | US-09-764-860-710 | Sequence 710, Appl |
| C 583 | 16 | 2.6 | 6171 | 12 | US-10-311-455-1987 | Sequence 1987, Ap | C 656 | 16 | 2.6 | 31885 | 10 | US-09-764-877-2530 | Sequence 2530, Ap |
| C 584 | 16 | 2.6 | 6182 | 12 | US-10-311-455-1987 | Sequence 1987, Ap | C 657 | 16 | 2.6 | 31885 | 10 | US-09-764-877-2541 | Sequence 2541, Ap |
| C 585 | 16 | 2.6 | 6274 | 11 | US-09-822-846-501 | Sequence 501, Appl | C 658 | 16 | 2.6 | 31885 | 10 | US-09-764-877-2541 | Sequence 2541, Ap |
| C 586 | 16 | 2.6 | 6277 | 12 | US-10-311-455-2013 | Sequence 2013, Ap | C 659 | 16 | 2.6 | 31885 | 11 | US-09-764-891-7211 | Sequence 7211, Ap |
| C 587 | 16 | 2.6 | 6285 | 10 | US-09-070-927A-415 | Sequence 415, Appl | C 660 | 16 | 2.6 | 31885 | 14 | US-10-074-095-775 | Sequence 775, Appl |
| C 588 | 16 | 2.6 | 6396 | 12 | US-10-311-455-2220 | Sequence 2220, Ap | C 661 | 16 | 2.6 | 32127 | 11 | US-09-764-891-6161 | Sequence 6161, Ap |
| C 589 | 16 | 2.6 | 6418 | 12 | US-10-311-455-296 | Sequence 296, Appl | C 662 | 16 | 2.6 | 32187 | 10 | US-09-764-847-1550 | Sequence 1550, Ap |
| C 590 | 16 | 2.6 | 6534 | 12 | US-10-311-455-444 | Sequence 444, Appl | C 663 | 16 | 2.6 | 32187 | 14 | US-10-092-154-1550 | Sequence 1550, Ap |
| C 591 | 16 | 2.6 | 6544 | 12 | US-10-311-455-520 | Sequence 520, Appl | C 664 | 16 | 2.6 | 32193 | 10 | US-09-764-847-1549 | Sequence 1549, Ap |
| C 592 | 16 | 2.6 | 6544 | 14 | US-10-239-676-46 | Sequence 46, Appl | C 665 | 16 | 2.6 | 32193 | 14 | US-10-092-154-1549 | Sequence 1549, Ap |
| C 593 | 16 | 2.6 | 6609 | 12 | US-10-311-455-1855 | Sequence 1855, Ap | C 666 | 16 | 2.6 | 32205 | 11 | US-09-764-891-10213 | Sequence 10213, A |
| C 594 | 16 | 2.6 | 6631 | 12 | US-10-240-453-213 | Sequence 213, Appl | C 667 | 16 | 2.6 | 32205 | 14 | US-10-205-428-1017 | Sequence 1017, Ap |
| C 595 | 16 | 2.6 | 6904 | 12 | US-10-311-455-185 | Sequence 185, Appl | C 668 | 16 | 2.6 | 32216 | 11 | US-09-764-891-9613 | Sequence 9613, Ap |
| C 596 | 16 | 2.6 | 6980 | 12 | US-10-311-455-426 | Sequence 426, Appl | C 669 | 16 | 2.6 | 32216 | 14 | US-10-205-428-536 | Sequence 536, Appl |
| C 597 | 16 | 2.6 | 7130 | 12 | US-10-311-455-778 | Sequence 778, Appl | C 670 | 16 | 2.6 | 33249 | 11 | US-09-764-891-7477 | Sequence 7477, Ap |
| C 598 | 16 | 2.6 | 7115 | 11 | US-09-764-891-9841 | Sequence 9841, Ap | C 671 | 16 | 2.6 | 34450 | 12 | US-10-293-832-3 | Sequence 3, Appl |
| C 599 | 16 | 2.6 | 7167 | 12 | US-10-311-455-373 | Sequence 373, Appl | C 672 | 16 | 2.6 | 34757 | 12 | US-10-293-832-22 | Sequence 22, Appl |
| C 600 | 16 | 2.6 | 7306 | 12 | US-10-311-455-1609 | Sequence 1609, Ap | C 673 | 16 | 2.6 | 35000 | 12 | US-09-793-807-10 | Sequence 10, Appl |

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|-----|----|-----|---------|----|----------------------|--------------------|-----|----|-----|-----|----|----------------------|--------------------|
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| 675 | 16 | 2.6 | 37973 | 12 | US-10-311-455-2169 | Sequence 2169, Ap | 748 | 15 | 2.4 | 275 | 10 | US-09-878-574-10888 | Sequence 10858, A |
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| 677 | 16 | 2.6 | 41936 | 10 | US-09-967-768A-1116 | Sequence 116, App | 750 | 15 | 2.4 | 277 | 10 | US-09-938-842A-3271 | Sequence 3271, Ap |
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| 679 | 16 | 2.6 | 51719 | 12 | US-10-353-150-2 | Sequence 2, Appli | 752 | 15 | 2.4 | 285 | 11 | US-09-918-995-18732 | Sequence 18732, A |
| 680 | 16 | 2.6 | 58837 | 10 | US-09-983-091A-5 | Sequence 5, Appli | 753 | 15 | 2.4 | 289 | 14 | US-10-043-487-210 | Sequence 210, App |
| 681 | 16 | 2.6 | 73334 | 12 | US-10-311-455-2098 | Sequence 2098, Ap | 754 | 15 | 2.4 | 311 | 9 | US-09-764-869-90 | Sequence 90, Appl |
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| 683 | 16 | 2.6 | 74862 | 14 | US-10-274-974-3 | Sequence 3, Appli | 756 | 15 | 2.4 | 312 | 10 | US-09-764-877-2859 | Sequence 2859, Ap |
| 684 | 16 | 2.6 | 92139 | 9 | US-09-918-686-1 | Sequence 1, Appli | 757 | 15 | 2.4 | 315 | 10 | US-09-963-865-2450 | Sequence 2450, Ap |
| 685 | 16 | 2.6 | 92139 | 12 | US-10-353-150-1 | Sequence 1, Appli | 758 | 15 | 2.4 | 318 | 13 | US-10-027-632-175506 | Sequence 175506, A |
| 686 | 16 | 2.6 | 113515 | 12 | US-10-311-455-2147 | Sequence 2147, Ap | 759 | 15 | 2.4 | 318 | 13 | US-10-027-632-175508 | Sequence 175508, A |
| 687 | 16 | 2.6 | 142299 | 11 | US-09-911-077A-14 | Sequence 14, Appl | 760 | 15 | 2.4 | 321 | 10 | US-09-736-457-1500 | Sequence 1500, Ap |
| 688 | 16 | 2.6 | 162025 | 12 | US-10-272-665-35 | Sequence 35, Appl | 761 | 15 | 2.4 | 321 | 10 | US-09-902-641-1500 | Sequence 1500, Ap |
| 689 | 16 | 2.6 | 162025 | 12 | US-10-272-665-36 | Sequence 36, Appl | 762 | 15 | 2.4 | 321 | 10 | US-09-849-626-1500 | Sequence 1500, Ap |
| 690 | 16 | 2.6 | 162025 | 12 | US-10-273-321-35 | Sequence 35, Appl | 763 | 15 | 2.4 | 321 | 12 | US-10-113-872-1500 | Sequence 1500, Ap |
| 691 | 16 | 2.6 | 162025 | 12 | US-10-273-321-36 | Sequence 36, Appl | 764 | 15 | 2.4 | 321 | 14 | US-10-017-754-1500 | Sequence 1500, Ap |
| 692 | 16 | 2.6 | 172637 | 9 | US-09-805-458A-3 | Sequence 3, Appli | 765 | 15 | 2.4 | 325 | 14 | US-10-198-846-11640 | Sequence 11640, A |
| 693 | 16 | 2.6 | 183337 | 14 | US-10-020-141-5 | Sequence 5, Appli | 766 | 15 | 2.4 | 327 | 10 | US-09-878-574-174 | Sequence 174, App |
| 694 | 16 | 2.6 | 202001 | 9 | US-09-734-674-3 | Sequence 3, Appli | 767 | 15 | 2.4 | 328 | 10 | US-09-764-847-267 | Sequence 267, App |
| 695 | 16 | 2.6 | 202001 | 14 | US-10-274-990-3 | Sequence 3, Appli | 768 | 15 | 2.4 | 328 | 14 | US-10-092-154-267 | Sequence 267, App |
| 696 | 16 | 2.6 | 260209 | 12 | US-10-025-966A-23 | Sequence 23, Appl | 769 | 15 | 2.4 | 338 | 11 | US-09-764-891-22 | Sequence 22, Appl |
| 697 | 16 | 2.6 | 260209 | 12 | US-10-265-071-23 | Sequence 23, Appl | 770 | 15 | 2.4 | 344 | 12 | US-09-814-353-1393 | Sequence 1393, Ap |
| 698 | 16 | 2.6 | 322101 | 12 | US-10-060-902-1 | Sequence 1, Appli | 771 | 15 | 2.4 | 344 | 12 | US-09-814-353-7756 | Sequence 7756, Ap |
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| 703 | 16 | 2.6 | 513509 | 11 | US-09-754-853A-4 | Sequence 4, Appli | 776 | 15 | 2.4 | 354 | 10 | US-09-954-456-916 | Sequence 916, App |
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| 706 | 16 | 2.6 | 786431 | 12 | US-10-412-277-3 | Sequence 3, Appli | 779 | 15 | 2.4 | 358 | 11 | US-09-991-936-569 | Sequence 569, App |
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| 711 | 16 | 2.6 | 1830121 | 14 | US-10-339-960-1 | Sequence 1, Appli | 784 | 15 | 2.4 | 377 | 9 | US-09-864-761-10289 | Sequence 10289, A |
| 712 | 16 | 2.6 | 2140405 | 13 | US-10-027-632-76212 | Sequence 76212, A | 785 | 15 | 2.4 | 377 | 13 | US-10-027-632-35752 | Sequence 35752, A |
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| 719 | 15 | 2.4 | 46 | 14 | US-10-085-906-252 | Sequence 25, App | 792 | 15 | 2.4 | 393 | 12 | US-09-880-107-2629 | Sequence 2629, App |
| 720 | 15 | 2.4 | 72 | 13 | US-08-781-986A-2728 | Sequence 2728, App | 793 | 15 | 2.4 | 393 | 12 | US-09-930-213-237 | Sequence 227, App |
| 721 | 15 | 2.4 | 105 | 10 | US-09-969-373-708 | Sequence 59, Appl | 794 | 15 | 2.4 | 398 | 9 | US-09-764-887-59 | Sequence 59, Appl |
| 722 | 15 | 2.4 | 118 | 10 | US-09-969-373-688 | Sequence 688, App | 795 | 15 | 2.4 | 398 | 14 | US-10-073-961-59 | Sequence 59, Appl |
| 723 | 15 | 2.4 | 145 | 11 | US-09-754-853A-350 | Sequence 350, App | 796 | 15 | 2.4 | 399 | 8 | US-10-198-846-3133 | Sequence 3133, Ap |
| 724 | 15 | 2.4 | 153 | 10 | US-09-867-701-9362 | Sequence 9362, App | 797 | 15 | 2.4 | 400 | 8 | US-08-781-986A-3912 | Sequence 3912, Ap |
| 725 | 15 | 2.4 | 156 | 10 | US-09-876-574-8380 | Sequence 8380, Ap | 798 | 15 | 2.4 | 400 | 11 | US-09-918-995-16704 | Sequence 16704, A |
| 726 | 15 | 2.4 | 165 | 9 | US-09-864-761-24065 | Sequence 24065, A | 799 | 15 | 2.4 | 401 | 14 | US-10-000-256A-77 | Sequence 77, Appl |
| 727 | 15 | 2.4 | 165 | 10 | US-09-974-300-3766 | Sequence 3766, App | 800 | 15 | 2.4 | 404 | 9 | US-09-795-668-1416 | Sequence 1416, App |
| 728 | 15 | 2.4 | 167 | 9 | US-09-563-817-455 | Sequence 455, App | 801 | 15 | 2.4 | 404 | 9 | US-09-795-666-1416 | Sequence 1416, App |
| 729 | 15 | 2.4 | 175 | 9 | US-09-815-242-2787 | Sequence 2787, App | 802 | 15 | 2.4 | 404 | 10 | US-09-946-807-1416 | Sequence 1416, App |
| 730 | 15 | 2.4 | 182 | 9 | US-09-848-889-8 | Sequence 8, Appli | 803 | 15 | 2.4 | 408 | 11 | US-09-918-995-33114 | Sequence 33114, A |
| 731 | 15 | 2.4 | 182 | 12 | US-10-100-982-8 | Sequence 8, Appli | 804 | 15 | 2.4 | 410 | 10 | US-09-796-692-5301 | Sequence 5301, Ap |
| 732 | 15 | 2.4 | 192 | 10 | US-09-783-590-9913 | Sequence 3913, App | 805 | 15 | 2.4 | 410 | 14 | US-10-040-862-5301 | Sequence 5301, Ap |
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| 735 | 15 | 2.4 | 201 | 10 | US-09-969-373-1047 | Sequence 1047, App | 808 | 15 | 2.4 | 414 | 10 | US-09-867-701-2169 | Sequence 2169, App |
| 736 | 15 | 2.4 | 215 | 12 | US-09-930-213-629 | Sequence 629, App | 809 | 15 | 2.4 | 414 | 10 | US-09-960-352-5205 | Sequence 5205, App |
| 737 | 15 | 2.4 | 218 | 14 | US-10-106-698-1739 | Sequence 1739, App | 810 | 15 | 2.4 | 414 | 11 | US-09-918-995-36730 | Sequence 36730, A |
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| 741 | 15 | 2.4 | 232 | 12 | US-10-099-926-1302 | Sequence 1302, App | 814 | 15 | 2.4 | 416 | 9 | US-09-795-668-1484 | Sequence 1484, App |
| 742 | 15 | 2.4 | 232 | 13 | US-10-033-528-1302 | Sequence 1302, App | 815 | 15 | 2.4 | 416 | 10 | US-09-946-807-1484 | Sequence 1484, App |
| 743 | 15 | 2.4 | 244 | 10 | US-09-876-574-2475 | Sequence 2475, App | 816 | 15 | 2.4 | 416 | 11 | US-09-918-995-36448 | Sequence 36448, A |
| 744 | 15 | 2.4 | 248 | 10 | US-09-728-444-1060 | Sequence 1060, App | 817 | 15 | 2.4 | 417 | 10 | US-09-867-701-3243 | Sequence 3243, App |
| 745 | 15 | 2.4 | 256 | 8 | US-08-781-986A-3084 | Sequence 3084, App | 818 | 15 | 2.4 | 418 | 12 | US-09-960-706-1172 | Sequence 1172, App |
| 746 | 15 | 2.4 | 258 | 14 | US-10-198-846-10062 | Sequence 10062, A | 819 | 15 | 2.4 | 419 | 10 | US-09-960-352-11234 | Sequence 11234, A |

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| C 820 | 15 | 2.4 | 419 | 10 | US-09-796-692-5814 | Sequence 5814, Ap | C 893 | 15 | 2.4 | 476 | 10 | US-09-880-107-2439 | Sequence 2439, Ap |
| C 821 | 15 | 2.4 | 419 | 14 | US-10-040-862-5814 | Sequence 5814, Ap | C 894 | 15 | 2.4 | 477 | 11 | US-09-918-995-26508 | Sequence 26508, A |
| C 822 | 15 | 2.4 | 419 | 14 | US-10-102-524-693 | Sequence 693, App | C 895 | 15 | 2.4 | 478 | 10 | US-09-764-877-3371 | Sequence 3371, Ap |
| C 823 | 15 | 2.4 | 421 | 10 | US-09-880-107-1190 | Sequence 1190, Ap | C 896 | 15 | 2.4 | 478 | 10 | US-09-764-877-3372 | Sequence 3372, Ap |
| C 824 | 15 | 2.4 | 422 | 14 | US-10-000-2564-773 | Sequence 773, Appl | C 897 | 15 | 2.4 | 478 | 10 | US-09-796-692-3440 | Sequence 3440, Ap |
| C 825 | 15 | 2.4 | 425 | 11 | US-09-918-995-34061 | Sequence 34061, A | C 898 | 15 | 2.4 | 478 | 14 | US-10-040-862-3440 | Sequence 3440, Ap |
| C 826 | 15 | 2.4 | 428 | 13 | US-10-027-632-43938 | Sequence 43938, A | C 899 | 15 | 2.4 | 480 | 11 | US-09-918-995-15593 | Sequence 15593, A |
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| C 832 | 15 | 2.4 | 435 | 13 | US-10-027-632-180318 | Sequence 180318, A | C 905 | 15 | 2.4 | 481 | 13 | US-10-027-632-33915 | Sequence 33915, Ap |
| C 833 | 15 | 2.4 | 435 | 13 | US-10-027-632-180319 | Sequence 180319, A | C 906 | 15 | 2.4 | 482 | 11 | US-09-918-995-15919 | Sequence 15919, A |
| C 834 | 15 | 2.4 | 436 | 11 | US-09-918-995-35353 | Sequence 35353, A | C 907 | 15 | 2.4 | 483 | 12 | US-09-918-995-13333 | Sequence 13333, Ap |
| C 835 | 15 | 2.4 | 436 | 13 | US-10-027-632-72001 | Sequence 72001, A | C 908 | 15 | 2.4 | 483 | 12 | US-09-918-995-7697 | Sequence 7697, Ap |
| C 836 | 15 | 2.4 | 436 | 13 | US-10-027-632-84282 | Sequence 84282, A | C 909 | 15 | 2.4 | 484 | 11 | US-09-918-995-24543 | Sequence 24543, A |
| C 837 | 15 | 2.4 | 436 | 13 | US-10-027-632-933508 | Sequence 933508, A | C 910 | 15 | 2.4 | 485 | 10 | US-09-867-701-5385 | Sequence 5385, Ap |
| C 838 | 15 | 2.4 | 439 | 13 | US-10-027-632-40303 | Sequence 40303, A | C 911 | 15 | 2.4 | 488 | 11 | US-09-918-995-24404 | Sequence 24404, A |
| C 839 | 15 | 2.4 | 440 | 12 | US-10-027-632-315228 | Sequence 315228, A | C 912 | 15 | 2.4 | 489 | 12 | US-09-814-353-14141 | Sequence 14141, A |
| C 840 | 15 | 2.4 | 440 | 12 | US-09-960-706-851 | Sequence 851, App | C 913 | 15 | 2.4 | 491 | 14 | US-10-157-031-318 | Sequence 318, App |
| C 841 | 15 | 2.4 | 441 | 13 | US-10-027-632-55652 | Sequence 55652, A | C 914 | 15 | 2.4 | 491 | 11 | US-09-918-995-19429 | Sequence 19429, A |
| C 842 | 15 | 2.4 | 441 | 13 | US-10-027-632-80854 | Sequence 80854, A | C 915 | 15 | 2.4 | 496 | 11 | US-09-918-995-6902 | Sequence 6902, Ap |
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| C 845 | 15 | 2.4 | 441 | 13 | US-10-027-632-315228 | Sequence 315228, A | C 918 | 15 | 2.4 | 500 | 11 | US-09-991-936-581 | Sequence 581, App |
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| C 847 | 15 | 2.4 | 443 | 10 | US-09-960-352-3833 | Sequence 3833, Ap | C 920 | 15 | 2.4 | 500 | 13 | US-10-027-632-42859 | Sequence 42859, A |
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| C 851 | 15 | 2.4 | 446 | 13 | US-10-027-632-62815 | Sequence 62815, A | C 924 | 15 | 2.4 | 501 | 13 | US-10-027-632-323262 | Sequence 323262, A |
| C 852 | 15 | 2.4 | 446 | 13 | US-10-027-632-64379 | Sequence 64379, A | C 925 | 15 | 2.4 | 502 | 13 | US-10-027-632-6481 | Sequence 6481, Ap |
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| C 858 | 15 | 2.4 | 451 | 11 | US-09-551-621-107 | Sequence 107, App | C 931 | 15 | 2.4 | 504 | 13 | US-10-027-632-285200 | Sequence 285200, A |
| C 859 | 15 | 2.4 | 451 | 12 | US-10-124-805-107 | Sequence 107, App | C 932 | 15 | 2.4 | 504 | 13 | US-10-027-632-285201 | Sequence 285201, A |
| C 860 | 15 | 2.4 | 451 | 13 | US-10-007-805-107 | Sequence 107, App | C 933 | 15 | 2.4 | 504 | 13 | US-10-027-632-285201 | Sequence 285201, A |
| C 861 | 15 | 2.4 | 451 | 14 | US-10-076-622-107 | Sequence 107, App | C 934 | 15 | 2.4 | 505 | 12 | US-10-102-524-736 | Sequence 736, App |
| C 862 | 15 | 2.4 | 453 | 10 | US-09-867-701-4766 | Sequence 4766, Ap | C 935 | 15 | 2.4 | 505 | 13 | US-10-027-632-18080 | Sequence 18080, A |
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| C 865 | 15 | 2.4 | 456 | 13 | US-10-027-632-86542 | Sequence 86542, A | C 938 | 15 | 2.4 | 507 | 13 | US-10-027-632-195208 | Sequence 195208, A |
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| C 867 | 15 | 2.4 | 461 | 11 | US-09-918-995-8996 | Sequence 2996, Ap | C 940 | 15 | 2.4 | 507 | 13 | US-10-027-632-246205 | Sequence 246205, A |
| C 868 | 15 | 2.4 | 462 | 13 | US-10-027-632-313576 | Sequence 313576, A | C 941 | 15 | 2.4 | 509 | 13 | US-10-027-632-246206 | Sequence 246206, A |
| C 869 | 15 | 2.4 | 463 | 9 | US-10-027-632-313577 | Sequence 313577, A | C 942 | 15 | 2.4 | 509 | 13 | US-10-027-632-51389 | Sequence 51389, A |
| C 870 | 15 | 2.4 | 463 | 11 | US-09-770-444-360 | Sequence 360, App | C 943 | 15 | 2.4 | 511 | 13 | US-10-027-632-277831 | Sequence 277831, A |
| C 871 | 15 | 2.4 | 463 | 11 | US-09-764-891-5392 | Sequence 5392, Ap | C 944 | 15 | 2.4 | 511 | 13 | US-10-027-632-277831 | Sequence 277831, A |
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| C 875 | 15 | 2.4 | 464 | 10 | US-09-736-457-3 | Sequence 3 | C 948 | 15 | 2.4 | 516 | 13 | US-10-027-632-214965 | Sequence 214965, A |
| C 876 | 15 | 2.4 | 464 | 10 | US-09-902-941-3 | Sequence 3, Appl | C 949 | 15 | 2.4 | 516 | 13 | US-10-027-632-317369 | Sequence 317369, A |
| C 877 | 15 | 2.4 | 464 | 10 | US-09-849-526-3 | Sequence 3, Appl | C 950 | 15 | 2.4 | 516 | 13 | US-10-027-632-317370 | Sequence 317370, A |
| C 878 | 15 | 2.4 | 464 | 11 | US-09-476-300-3 | Sequence 3, Appl | C 951 | 15 | 2.4 | 517 | 13 | US-10-027-632-324715 | Sequence 324715, A |
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| C 892 | 15 | 2.4 | 475 | 11 | US-09-918-995-15305 | Sequence 15305, A | C 965 | 15 | 2.4 | 530 | 13 | US-10-027-632-134620 | Sequence 134620, A |

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C 996 15 2.4 548 13 US-10-027-632-179530 Sequence 179530, App
C 997 15 2.4 548 13 US-10-027-632-316733 Sequence 316733, App
C 998 15 2.4 549 10 US-09-974-300-3024 Sequence 3024, App
C 999 15 2.4 550 11 US-09-991-936-1413 Sequence 1413, App
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ALIGNMENTS

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RESULT 1
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; Sequence 1, Application US/10010160
; Publication No. US20030103999A1
; GENERAL INFORMATION:
; APPLICANT: Rosey, Everett L.
; APPLICANT: Strugnell, Richard A.
; APPLICANT: Good, Robert T.
; APPLICANT: King, Kendall W.
; TITLE OF INVENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR
; FILE REFERENCE: DAV110.001AUS
; CURRENT APPLICATION NUMBER: US/10/010,160
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: AU P1381
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/249,596
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Lamsonia intracellularis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(621)
US-10-010-160-1

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Best Local Similarity 100.0%; Pred. No. 7e-306;
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TCTGAAGGAGTGTCCCTAATTCAGAGAGGTTACTTAAGATTGACTTACGACGAGG 120
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RESULT 2
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; Sequence 47579, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47579
; LENGTH: 622

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TYPE: DNA
ORGANISM: Human
US-10-027-632-47579

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Db 317 GTTTTAAATTAAATGAG 336

RESULT 3
US-10-027-632-75231
Sequence 75231, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75231
LENGTH: 624
TYPE: DNA
ORGANISM: Human
US-10-027-632-75231

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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Sequence 313525, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.139
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 313525
LENGTH: 624
TYPE: DNA
ORGANISM: Human
US-10-027-632-313525

Query Match
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 GTTTTAAATTAAATGAG 371
Db 319 GTTTTAAATTAAATGAG 338

RESULT 5
US-10-060-036-1428/c
Sequence 1428, Application US/10060036
Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yugu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1428
LENGTH: 340
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 308
OTHER INFORMATION: n = A,T,C or G
US-10-060-036-1428

Query Match
Best Local Similarity 3.1%; Score 19; DB 14; Length 340;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 261 AGCTATTTTATGATGCCA 279
Db 307 AGCTATTTTATGATGCCA 289

RESULT 6
US-09-864-761-5935/c
Sequence 5935, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23

```
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 5935
/ LENGTH: 390
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC004896.1
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.4
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
/ OTHER INFORMATION: EXPRESSED IN HEP4, SIGNAL = 5
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.6
/ US-09-864-761-5935

Query Match          3.1%; Score 19; DB 9; Length 390;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      228 ATATGCTTATTATTAT 246
Db      79 ATATGCTTATTATTAT 61
```

```
RESULT 7
US-10-027-632-220095
/ Sequence 220095, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
```

```
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 220095
/ LENGTH: 636
/ TYPE: DNA
/ ORGANISM: Human
/ US-10-027-632-220095

Query Match          3.1%; Score 19; DB 13; Length 636;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      183 TATTTTACAGATCATTT 201
Db      605 TATTTTACAGATCATTT 623
```

```
RESULT 8
US-10-027-632-220096
/ Sequence 220096, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 220096
/ LENGTH: 636
/ TYPE: DNA
/ ORGANISM: Human
/ US-10-027-632-220096
```

```
Query Match          3.1%; Score 19; DB 13; Length 636;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      183 TATTTTACAGATCATTT 201
Db      605 TATTTTACAGATCATTT 623
```

RESULT 9

```
US-10-027-632-220097
; Sequence 220097, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220097
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220097
```

```
Query Match          3.1%; Score 19; DB 13; Length 636;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      183 TATTTTACAGATCATTT 201
        ||||||||||||||||
Db       605 TATTTTACAGATCATTT 623
```

```
RESULT 10
US-10-027-632-220098
; Sequence 220098, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220098
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220098
```

```
Query Match          3.1%; Score 19; DB 13; Length 636;
```

```
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      183 TATTTTACAGATCATTT 201
        ||||||||||||||||
Db       605 TATTTTACAGATCATTT 623
```

```
RESULT 11
US-10-027-632-220099
; Sequence 220099, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220099
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220099
```

```
Query Match          3.1%; Score 19; DB 13; Length 636;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      183 TATTTTACAGATCATTT 201
        ||||||||||||||||
Db       605 TATTTTACAGATCATTT 623
```

```
RESULT 12
US-10-027-632-220100
; Sequence 220100, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
```

```

; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220100
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220100

Query Match
Best Local Similarity 100.0%; Score 19; DB 13; Length 636;
Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TATTTTACGAATCATTT 201
    |||||||
Db 605 TATTTTACGAATCATTT 623

RESULT 13
US-10-313-542-28
; Sequence 28, Application US/10313542
; Publication No. US20030120057A1
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/10/313,542
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US/09/495,050
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030120057A1 647628CT1
US-10-313-542-28

Query Match
Best Local Similarity 100.0%; Score 19; DB 14; Length 948;
Pred. No. 31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 AGCTATTTTATGATGCCA 279
    |||||||
Db 678 AGCTATTTTATGATGCCA 696

RESULT 14
US-09-887-527-53/c
; Sequence 53, Application US/09887527
; Publication No. US20030055006A1
; GENERAL INFORMATION:
; APPLICANT: SIEMEISTER, GERHARD
; APPLICANT: HABEREY, MARTIN
; APPLICANT: THIERAUCH, KARL-HEINZ
; TITLE OF INVENTION: COMBINATIONS AND COMPOSITIONS WHICH INTERFERE WITH
; TITLE OF INVENTION: VEGF/VEGF AND ANGIOPOIETIN/TIE RECEPTOR FUNCTION
; TITLE OF INVENTION: AND THEIR USE
; FILE REFERENCE: SCH-1815
; CURRENT APPLICATION NUMBER: US/09/887,527
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE 00250194.8
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: DE 00250214.4
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
```

```

; SEQ ID NO 53
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-887-527-53

Query Match
Best Local Similarity 100.0%; Score 19; DB 11; Length 989;
Pred. No. 31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 ATTACTTTTATGCTGTT 300
    |||||||
Db 771 ATTACTTTTATGCTGTT 753

RESULT 15
US-09-764-891-8977
; Sequence 8977, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8977
; LENGTH: 2422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8977

Query Match
Best Local Similarity 100.0%; Score 19; DB 11; Length 2422;
Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 ATTACTTTTATGCTGTT 300
    |||||||
Db 1593 ATTACTTTTATGCTGTT 1611

RESULT 16
US-09-764-891-8978
; Sequence 8978, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8978
; LENGTH: 2422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8978

Query Match
Best Local Similarity 100.0%; Score 19; DB 11; Length 2422;
Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 ATTACTTTTATGCTGTT 300
    |||||||
Db 1593 ATTACTTTTATGCTGTT 1611

RESULT 17
US-10-044-090-452
```


Sequence 452, Application US/10044090
Publication No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 452
LENGTH: 3318
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 199489.1
NAME/KEY: unsure
LOCATION: 1255, 1299
OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-452

Query Match 3.1%; Score 19; DB 13; Length 3318;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 261 AGCTATTATTGATGCCA 279
Db 1507 AGCTATTATTGATGCCA 1525

RESULT 18
US-09-764-891-8976
Sequence 8976, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8976
LENGTH: 10468
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-8976

Query Match 3.1%; Score 19; DB 11; Length 10468;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 ATTACTTTTATGCTGTT 300
Db 7435 ATTACTTTTATGCTGTT 7453

RESULT 19
US-09-764-891-8979
Sequence 8979, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8979

LENGTH: 10468
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-8979

Query Match 3.1%; Score 19; DB 11; Length 10468;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 ATTACTTTTATGCTGTT 300
Db 7435 ATTACTTTTATGCTGTT 7453

RESULT 20
US-10-007-078-10
Sequence 10, Application US/10007078
Publication No. US20030105042A1
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF EIF2C1 EXPRESSION
FILE REFERENCE: RTS-0236
CURRENT APPLICATION NUMBER: US/10/007,078
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
LENGTH: 42500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 18344-18443, 25149-25248, 27228-27327, 27357
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: intron
LOCATION: (820)...(5800)
OTHER INFORMATION: Intron 1
NAME/KEY: intron
LOCATION: (5985)...(9929)
OTHER INFORMATION: Intron 2
NAME/KEY: intron
LOCATION: (10051)...(10469)
OTHER INFORMATION: Intron 3
NAME/KEY: intron
LOCATION: (10652)...(11046)
OTHER INFORMATION: Intron 4
NAME/KEY: intron
LOCATION: (11184)...(11409)
OTHER INFORMATION: Intron 5
NAME/KEY: intron
LOCATION: (11545)...(11687)
OTHER INFORMATION: Intron 6
NAME/KEY: intron
LOCATION: (11776)...(12494)
OTHER INFORMATION: Intron 7
NAME/KEY: intron
LOCATION: (12643)...(18653)
OTHER INFORMATION: Intron 8
NAME/KEY: intron
LOCATION: (18774)...(19127)
OTHER INFORMATION: Intron 9
NAME/KEY: intron
LOCATION: (19251)...(19383)
OTHER INFORMATION: Intron 10
NAME/KEY: intron
LOCATION: (19518)...(24114)
OTHER INFORMATION: Intron 11
NAME/KEY: intron
LOCATION: (24300)...(30976)
OTHER INFORMATION: Intron 12
NAME/KEY: intron
LOCATION: (31137)...(31318)
OTHER INFORMATION: Intron 13

```
NAME/KEY: intron
LOCATION: (31410)...(32482)
OTHER INFORMATION: Intron 14
NAME/KEY: intron
LOCATION: (32678)...(34727)
OTHER INFORMATION: Intron 15
NAME/KEY: intron
LOCATION: (34863)...(35456)
OTHER INFORMATION: Intron 16
NAME/KEY: intron
LOCATION: (35559)...(36189)
OTHER INFORMATION: Intron 17
NAME/KEY: intron
LOCATION: (36390)...(36633)
OTHER INFORMATION: Intron 18
NAME/KEY: intron
LOCATION: (41435)...(42500)
OTHER INFORMATION: Intron 19
US-10-007-078-10
```

```
Query Match      3.1% Score 19; DB 14; Length 42500;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      352 GTTTTAAATTAAATGA 370
DB      23190 GTTTTAAATTAAATGA 23208
```

```
RESULT 21
US-10-144-649A-746/c
Sequence 746, Application US/10144649A
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.475C11
CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 746
LENGTH: 161280
TYPE: DNA
ORGANISM: Homo sapiens
US-10-144-649A-746
```

```
Query Match      3.1% Score 19; DB 14; Length 161280;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      230 ATGCTTATTATTATATG 248
DB      113647 ATGCTTATTATTATATG 113629
```

```
RESULT 22
US-09-754-853A-4
Sequence 4, Application US/09754853A
Publication No. US20030005491A1
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-10(15810)B
```

```
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIORITY APPLICATION NUMBER: US 60/174,880
PRIORITY FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 4
LENGTH: 513509
TYPE: DNA
ORGANISM: glycine max
FEATURE:
NAME/KEY: CDS
LOCATION: (11805)..(113968), (114684)..(115204)
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(513509)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
US-09-754-853A-4
```

```
Query Match      3.1% Score 19; DB 11; Length 513509;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      352 GTTTTAAATTAAATGA 370
DB      425451 GTTTTAAATTAAATGA 425469
```

```
RESULT 23
US-09-795-668-1/c
Sequence 1, Application US/09795668
Patent No. US2002004577A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Guicher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIORITY APPLICATION NUMBER: US 09/515,716
PRIORITY FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503841
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: r=g or a
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: y=c/u or c
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: s=g or c
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: w=a or t/u
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: b=g or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: d=a or g or t/u
```

```
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h=a or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: n=a or g or c or t/u
US-09-795-668-1
```

```
Query Match 3.1%; Score 19; DB 9; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 228 ATATGCTTTATTTATTTAT 246
Db 963911 ATATGCTTTATTTATTTAT 963893
```

RESULT 24

```
US-09-795-686-1/c
Sequence 1, Application US/09795666
Patent No. US20020094954A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinhorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503841
```

```
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: r=g or a
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h=a or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
```

```
OTHER INFORMATION: n=a or g or c or t/u
US-09-795-686-1
```

```
Query Match 3.1%; Score 19; DB 9; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 228 ATATGCTTTATTTATTTAT 246
Db 963911 ATATGCTTTATTTATTTAT 963893
```

RESULT 25

```
US-09-946-807-1/c
Sequence 1, Application US/09946807
Patent No. US20020165144A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinhorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503841
```

```
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: r=g or a
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h=a or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
```

```
OTHER INFORMATION: v=a or g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: n=a or g or c or t/u
US-09-946-807-1
```

```
Query Match          3.1%: Score 19; DB 10; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      228 ATATGCTTATTTATTTAT 246
      |||||||
Db      963911 AATGCTTATTTATTTAT 963893
```

```
RESULT 26
US-10-067-514-1
; Sequence 1, Application US/10067514
; Publication No. US20030054531A1
```

```
GENERAL INFORMATION:
APPLICANT: Gtelarsdotcitr, Solveig
APPLICANT: Jonsdotcitr, Sif
APPLICANT: Reynisdotcitr, Sigridur Th.
TITLE OF INVENTION: HUMAN STROKE GENE
FILE REFERENCE: 2345.2010-003
CURRENT APPLICATION NUMBER: US/10/067,514
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US 09/811/352
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1691139
TYPE: DNA
ORGANISM: Human
US-10-067-514-1
```

```
Query Match          3.1%: Score 19; DB 14; Length 1691139;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      169 ACAATTTCTACTATATTT 187
      |||||||
Db      681945 ACAATTTCTACTATATTT 681963
```

```
RESULT 27
US-10-027-632-174961/c
; Sequence 174961, Application US/10027632
; GENERAL INFORMATION:
```

```
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
```

```
SEQ ID NO 174961
LENGTH: 3186778
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(3186778)
OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961
```

```
Query Match          3.1%: Score 19; DB 13; Length 3186778;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      360 ATTTAAATGAGATTAATTT 378
      |||||||
Db      57048 ATTTAAATGAGATTAATTT 57030
```

```
RESULT 28
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
```

```
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
```

```
Query Match          3.1%: Score 19; DB 10; Length 3309400;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      376 TTTAATATATTAAGGCT 394
      |||||||
Db      1835974 TTTAATATATTAAGGCT 1835992
```

```
RESULT 29
US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
```

```
GENERAL INFORMATION:
APPLICANT: Biogenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
```

```
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
```

```
Query Match          3.1%; Score 19; DB 12; Length 3673778;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      372 TAAATTATATATATAA 390
Db      2991275 TAAATTATATATATAA 2991257
```

```
RESULT 30
US-09-878-574-67
; Sequence 67, Application US/09878574
; Patent No. US20020110548A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
```

```
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
```

```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
```

```
; FILE REFERENCE: 38-21(15401)B
```

```
; CURRENT APPLICATION NUMBER: US/09/878,574
```

```
; CURRENT FILING DATE: 2001-12-21
```

```
; PRIOR APPLICATION NUMBER: 09/333,535
```

```
; PRIOR FILING DATE: 1999-06-14
```

```
; NUMBER OF SEQ ID NOS: 15775
```

```
; SEQ ID NO 67
```

```
; LENGTH: 393
```

```
; TYPE: DNA
```

```
; ORGANISM: Glycine max
```

```
; FEATURE:
```

```
; NAME/KEY: unsure
```

```
; LOCATION: (1)..(393)
```

```
; OTHER INFORMATION: unsure at all n locations
```

```
; OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-E4
```

```
US-09-878-574-67
```

```
Query Match          2.9%; Score 18; DB 10; Length 393;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      353 TTTTAAATTTAAATGGA 370
Db      109 TTTTAAATTTAAATGGA 126
```

```
RESULT 31
US-10-027-632-134481
; Sequence 134481, Application US/10027632
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

```
; FILE REFERENCE: 108827.129
```

```
; CURRENT APPLICATION NUMBER: US/10/027,632
```

```
; PRIOR APPLICATION NUMBER: US 60/218,006
```

```
; PRIOR FILING DATE: 2000-07-12
```

```
; PRIOR APPLICATION NUMBER: US 60/198,676
```

```
; PRIOR FILING DATE: 2000-04-20
```

```
; PRIOR APPLICATION NUMBER: US 60/193,483
```

```
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
```

```
; PRIOR FILING DATE: 2000-02-24
```

```
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134481
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134481
```

```
Query Match          2.9%; Score 18; DB 13; Length 399;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      112 GCAGCAGGATGCTGGG 129
Db      317 GCAGCAGGATGCTGGG 334
```

```
RESULT 32
US-10-027-632-192884
; Sequence 192884, Application US/10027632
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

```
; FILE REFERENCE: 108827.129
```

```
; CURRENT APPLICATION NUMBER: US/10/027,632
```

```
; CURRENT FILING DATE: 2002-04-30
```

```
; PRIOR APPLICATION NUMBER: US 60/218,006
```

```
; PRIOR FILING DATE: 2000-07-12
```

```
; PRIOR APPLICATION NUMBER: US 60/198,676
```

```
; PRIOR FILING DATE: 2000-04-20
```

```
; PRIOR APPLICATION NUMBER: US 60/193,483
```

```
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
```

```
; PRIOR FILING DATE: 2000-02-24
```

```
; PRIOR APPLICATION NUMBER: US 60/167,363
```

```
; PRIOR FILING DATE: 1999-11-23
```

```
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```
; PRIOR FILING DATE: 1999-09-28
```

```
; PRIOR APPLICATION NUMBER: US 60/146,002
```

```
; PRIOR FILING DATE: 1999-08-09
```

```
; NUMBER OF SEQ ID NOS: 325720
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 192884
```

```
; LENGTH: 494
```

```
; TYPE: DNA
```

```
; ORGANISM: Human
```

```
US-10-027-632-192884
```

```
Query Match          2.9%; Score 18; DB 13; Length 494;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      173 TTTTCTATATATTTTA 190
Db      198 TTTTCTATATATTTTA 215
```

```
RESULT 33
US-09-728-445-491
; Sequence 491, Application US/09728445
; Patent No. US20020102543A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Friedrich, Glenn
```

```
; APPLICANT: Zamdrowicz, Brian
```

```
; APPLICANT: Sands, Arthur T.
```

```
; TITLE OF INVENTION: No. US20020102543A1 Mutated Mammalian Cells and
```

FILE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT APPLICATION NUMBER: US/09/728,445
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,358
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 491
LENGTH: 546
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(546)
OTHER INFORMATION: n = A,T,C or G
US-09-728-445-491

Query Match 2.9%; Score 18; DB 10; Length 546;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 GCTATTATTATGATGCCA 279
|||||
Db 114 GCTATTATTATGATGCCA 131

RESULT 34
US-09-864-761-14909/C
Sequence 14909, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 14909
LENGTH: 561
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009290.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
NAME/KEY: unsure
LOCATION: 95
NAME/KEY: unsure
LOCATION: 413
NAME/KEY: unsure
LOCATION: 414
NAME/KEY: unsure
LOCATION: 428
NAME/KEY: unsure
LOCATION: 434
NAME/KEY: unsure
LOCATION: 443
NAME/KEY: unsure
LOCATION: 465
US-09-864-761-14909

Query Match 2.9%; Score 18; DB 9; Length 561;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 TCATTGAAACAAATTTT 176
|||||
Db 502 TCATTGAAACAAATTTT 485

RESULT 35
US-10-027-632-215080
Sequence 215080, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 215080
LENGTH: 585
TYPE: DNA
ORGANISM: Human
US-10-027-632-215080

Query Match 2.9%; Score 18; DB 13; Length 585;
Best Local Similarity 100.0%; Pred. No. 97;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 228 ATATGCTTTATTATTTA 245
|||
Db 517 ATATGCTTTATTATTTA 534

RESULT 36
US-10-027-632-215081
; Sequence 215081, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215081
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215081

Query Match
Best Local Similarity 2.9%; Score 18; DB 13; Length 585;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 ATATGCTTTATTATTTA 245
|||
Db 517 ATATGCTTTATTATTTA 534

RESULT 37
US-10-027-632-192200/c
; Sequence 192200, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192200
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-192200

Query Match
Best Local Similarity 2.9%; Score 18; DB 13; Length 624;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AATTTAAATGAGCTAAA 375
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Db 499 AATTTAAATGAGCTAAA 482

RESULT 38
US-10-027-632-117860
; Sequence 117860, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117860
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-117860

Query Match
Best Local Similarity 2.9%; Score 18; DB 13; Length 1114;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 TTACTTTTATTTGCTGTT 300
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Db 377 TTACTTTTATTTGCTGTT 394

RESULT 39
US-09-764-870-30
; Sequence 30, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1440
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-764-870-30

Query Match 2.9%; Score 18; DB 9; Length 1440;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 AGGTTTTTAATTAAAT 367
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Db 1335 AGGTTTTTAATTAAAT 1352

RESULT 40
US-10-125-540-30
; Sequence 30, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-540-30

Query Match 2.9%; Score 18; DB 14; Length 1440;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 AGGTTTTTAATTAAAT 367
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Db 1335 AGGTTTTTAATTAAAT 1352

Search completed: October 8, 2003, 08:54:10
Job time : 242 secs

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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 06:22:36 ; Search time 1943 Seconds
(without alignments)
7780.434 Million cell updates/sec

Title: US-10-010-160-1
Perfect score: 622
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

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2: em_esthum:*
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19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 12 | 21 | 21 | 3.4 | 636 | 12 | BJ066017 | BJ066017 BU066017 |
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| 27 | 20 | 20 | 3.2 | 357 | 10 | BF481067 | BF481067 FW1_16_A0 |
| 28 | 20 | 20 | 3.2 | 364 | 9 | AW779697 | AW779697 hm84a01.x |
| 29 | 20 | 20 | 3.2 | 402 | 9 | AV503250 | AV503250 vm12f01.x |
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| 36 | 20 | 20 | 3.2 | 482 | 28 | AZ450611 | AZ450611 IM0249K19 |
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| 42 | 20 | 20 | 3.2 | 530 | 9 | AU263268 | AU263268 AU263268 |
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| 45 | 20 | 20 | 3.2 | 561 | 12 | BM257953 | BM257953 521848 MA |
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| 88 | 19 | 3.1 | 130 | 12 | B0331337 | B0331337 | 161 | 19 | 3.1 | 166 | 12 | B0338598 | B0338598 |
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| 97 | 19 | 3.1 | 132 | 12 | B0364551 | B0364551 | 170 | 19 | 3.1 | 167 | 12 | B0331433 | B0331433 |
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| 106 | 19 | 3.1 | 141 | 12 | B0331431 | B0331431 | 179 | 19 | 3.1 | 168 | 12 | B0392691 | B0392691 |
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| 136 | 19 | 3.1 | 163 | 12 | B0366012 | B0366012 | 209 | 19 | 3.1 | 174 | 12 | B0368286 | B0368286 |
| 137 | 19 | 3.1 | 164 | 12 | B0394345 | B0394345 | 210 | 19 | 3.1 | 174 | 12 | B0399460 | B0399460 |
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| 139 | 19 | 3.1 | 164 | 12 | B0331769 | B0331769 | 212 | 19 | 3.1 | 175 | 12 | B0393720 | B0393720 |
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|-----|----|-----|-----|----|----------|----------|----------|-------|----|-----|-----|----|-----------|-----------|-------------|
| 662 | 19 | 3.1 | 210 | 12 | BJ396559 | BJ396559 | BJ397353 | C 735 | 19 | 3.1 | 270 | 10 | BE180599 | BE180599 | KCJ-Rt0b |
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| 808 | 19 | 3.1 | 773 | 14 | CB318966 | CB318966 | AGENECOURT | 881 | 18 | 2.9 | 350 | 9 | AW523261 | AW523261 | UT-R-BOC- |
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| C 818 | 19 | 3.1 | 839 | 28 | BH680156 | BH680156 | BOMHB87TF | C 891 | 18 | 2.9 | 378 | 13 | BY672199 | BY672199 | BY672199 |
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| C 821 | 19 | 3.1 | 853 | 24 | BZ256996 | BZ256996 | CH230-283 | C 894 | 18 | 2.9 | 385 | 9 | AW528708 | AW528708 | UT-R-BO1- |
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| C 824 | 19 | 3.1 | 867 | 29 | BZ689101 | BZ689101 | PUBKX30TD | C 897 | 18 | 2.9 | 388 | 14 | T14822 | T14822 | cr8264.1amb |
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| C 827 | 19 | 3.1 | 883 | 28 | BH134374 | BH134374 | ENTNX02TF | C 900 | 18 | 2.9 | 396 | 9 | AA413502 | AA413502 | Fugu rubr |
| C 828 | 19 | 3.1 | 922 | 13 | BU749105 | BU749105 | CH3#024_G | C 901 | 18 | 2.9 | 396 | 29 | FR0038874 | FR0038874 | md97907.r1 |
| C 829 | 19 | 3.1 | 929 | 13 | BO712352 | BO712352 | AGENECOURT | C 902 | 18 | 2.9 | 397 | 14 | W62329 | W62329 | md97907.r1 |
| C 830 | 19 | 3.1 | 935 | 13 | BUI86626 | BUI86626 | AGENECOURT | C 903 | 18 | 2.9 | 399 | 14 | CB706708 | CB706708 | AMGNNUC:S |
| C 831 | 19 | 3.1 | 970 | 29 | CC287059 | CC287059 | CH261-160 | C 904 | 18 | 2.9 | 400 | 9 | AL1240859 | AL1240859 | qj99f06.x |
| C 832 | 19 | 3.1 | 973 | 13 | BO708148 | BO708148 | AGENECOURT | C 905 | 18 | 2.9 | 401 | 10 | BF116959 | BF116959 | uy92h11.y |
| C 833 | 19 | 3.1 | 989 | 12 | BM449637 | BM449637 | AGENECOURT | C 906 | 18 | 2.9 | 404 | 13 | BY225926 | BY225926 | BY225926 |
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| C 839 | 19 | 3.1 | 1113 | 12 | BM912527 | BM912527 | AGENECOURT | C 912 | 18 | 2.9 | 419 | 29 | AG231011 | AG231011 | Lotus jap |
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| C 847 | 18 | 2.9 | 169 | 13 | BUT66688 | BUT66688 | ik78b02.x | C 920 | 18 | 2.9 | 435 | 14 | CB792474 | CB792474 | AMGNNUC:N |
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| C 849 | 18 | 2.9 | 180 | 12 | BJ394413 | BJ394413 | AGENECOURT | C 922 | 18 | 2.9 | 437 | 29 | BZ885362 | BZ885362 | CH240-280 |
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| C 854 | 18 | 2.9 | 215 | 9 | AUI80215 | AUI80215 | AGENECOURT | C 927 | 18 | 2.9 | 449 | 10 | BE353533 | BE353533 | UG98f04.x |
| C 855 | 18 | 2.9 | 229 | 9 | AI810783 | AI810783 | tuz1a09.x | C 928 | 18 | 2.9 | 449 | 13 | BQ073848 | BQ073848 | fz31b12.x |
| C 856 | 18 | 2.9 | 233 | 28 | AQ425600 | AQ425600 | CITBI-EI- | C 929 | 18 | 2.9 | 449 | 14 | T15226 | T15226 | crs820.1amb |
| C 857 | 18 | 2.9 | 234 | 28 | AQ425605 | AQ425605 | CITBI-EI- | C 930 | 18 | 2.9 | 449 | 28 | AO561327 | AO561327 | HS-5371_A |
| C 858 | 18 | 2.9 | 247 | 28 | AQ424403 | AQ424403 | CITBI-EI- | C 931 | 18 | 2.9 | 452 | 28 | AO111919 | AO111919 | CTF-HSP-2 |
| C 859 | 18 | 2.9 | 249 | 9 | AA725958 | AA725958 | v085f04.r | C 932 | 18 | 2.9 | 455 | 28 | AQ282539 | AQ282539 | RCPI11-2G |
| C 860 | 18 | 2.9 | 254 | 28 | AO631375 | AO631375 | RCPI-11-4 | C 933 | 18 | 2.9 | 463 | 13 | BU097888 | BU097888 | Y46121G04 |
| C 861 | 18 | 2.9 | 259 | 9 | AI707761 | AI707761 | as35b05.x | C 934 | 18 | 2.9 | 463 | 18 | AQ112925 | AQ112925 | CIT-HSP-2 |
| C 862 | 18 | 2.9 | 263 | 14 | N74637 | N74637 | zass5603.s1 | C 935 | 18 | 2.9 | 464 | 28 | AQ286463 | AQ286463 | RCPI11-80 |
| C 863 | 18 | 2.9 | 303 | 28 | B14762 | B14762 | 342P5_TV_CI | C 936 | 18 | 2.9 | 466 | 9 | AI276056 | AI276056 | q169d03.x |
| C 864 | 18 | 2.9 | 304 | 10 | BE250230 | BE250230 | BB250230 | C 937 | 18 | 2.9 | 467 | 9 | AM669771 | AM669771 | 113318_MA |
| C 865 | 18 | 2.9 | 304 | 10 | BB363779 | BB363779 | BB363779 | C 938 | 18 | 2.9 | 471 | 10 | BE656423 | BE656423 | UT-M-BHO- |
| C 866 | 18 | 2.9 | 311 | 9 | AI695002 | AI695002 | w45c04.x | C 939 | 18 | 2.9 | 474 | 28 | AZ016432 | AZ016432 | RCPI-23-2 |
| C 867 | 18 | 2.9 | 312 | 9 | AI072906 | AI072906 | UI-R-YO-m | C 940 | 18 | 2.9 | 475 | 9 | AA542476 | AA542476 | fa07f12.b |
| C 868 | 18 | 2.9 | 315 | 12 | BM162759 | BM162759 | EST65282 | C 941 | 18 | 2.9 | 477 | 10 | BB785439 | BB785439 | BB785439 |
| C 869 | 18 | 2.9 | 319 | 9 | AM335596 | AM335596 | S49H12_AG | C 942 | 18 | 2.9 | 477 | 29 | TA219A04P | TA219A04P | T.brycel |
| C 870 | 18 | 2.9 | 320 | 9 | AU282329 | AU282329 | BOGIVSITF | C 943 | 18 | 2.9 | 479 | 12 | BM169391 | BM169391 | EST571914 |
| C 871 | 18 | 2.9 | 323 | 28 | BH496688 | BH496688 | BOGIVSITF | C 944 | 18 | 2.9 | 481 | 9 | AA794789 | AA794789 | v064a10.r |
| C 872 | 18 | 2.9 | 325 | 28 | AZ581509 | AZ581509 | IM0370N17 | C 945 | 18 | 2.9 | 481 | 28 | BM7520 | BM7520 | RCPI11-29E1 |
| C 873 | 18 | 2.9 | 332 | 9 | AA004082 | AA004082 | mg81g06.r | C 946 | 18 | 2.9 | 483 | 13 | BM165523 | BM165523 | EST568046 |
| C 874 | 18 | 2.9 | 336 | 28 | BH730560 | BH730560 | BOHVM27TR | C 947 | 18 | 2.9 | 483 | 14 | W67012 | W67012 | me29h10.r1 |
| C 875 | 18 | 2.9 | 342 | 14 | H38810 | H38810 | YP61d06.s1 | C 948 | 18 | 2.9 | 486 | 28 | BH451451 | BH451451 | BOHFT13TR |
| C 876 | 18 | 2.9 | 342 | 28 | AQ283991 | AQ283991 | RCPI11-86 | C 949 | 18 | 2.9 | 487 | 10 | CB726437 | CB726437 | AMGNNUC:S |
| C 877 | 18 | 2.9 | 343 | 10 | BB165372 | BB165372 | RCPI11-86 | C 950 | 18 | 2.9 | 488 | 10 | BF761314 | BF761314 | RC2-CS001 |
| C 878 | 18 | 2.9 | 344 | 14 | N75694 | N75694 | YWS2a02.r1 | C 951 | 18 | 2.9 | 488 | 29 | BZ278364 | BZ278364 | CH230-297 |
| C 879 | 18 | 2.9 | 345 | 9 | AA611334 | AA611334 | vm98e03.r | C 952 | 18 | 2.9 | 492 | 10 | BF635240 | BF635240 | NF062A10D |
| C 880 | 18 | 2.9 | 347 | 14 | H48536 | H48536 | YQ78C06.s1 | C 953 | 18 | 2.9 | 493 | 14 | W59478 | W59478 | md62f03.r1 |

| | | | | | | |
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| C 954 | 18 | 2.9 | 494 | 9 | AL385534 | AL385534 |
| C 955 | 18 | 2.9 | 498 | 28 | AO871044 | AO871044 |
| C 956 | 18 | 2.9 | 499 | 14 | CB712207 | CB712207 |
| C 957 | 18 | 2.9 | 502 | 14 | CA927699 | CA927699 |
| C 958 | 18 | 2.9 | 503 | 9 | AA645383 | AA645383 |
| C 959 | 18 | 2.9 | 504 | 9 | AA108018 | AA108018 |
| C 960 | 18 | 2.9 | 506 | 9 | AI475347 | AI475347 |
| C 961 | 18 | 2.9 | 507 | 28 | BZ161613 | BZ161613 |
| C 962 | 18 | 2.9 | 510 | 18 | BA6932 | BA6932 |
| C 963 | 18 | 2.9 | 510 | 28 | BH766152 | BH766152 |
| C 964 | 18 | 2.9 | 511 | 14 | CB222203 | CB222203 |
| C 965 | 18 | 2.9 | 511 | 28 | AO615559 | AO615559 |
| C 966 | 18 | 2.9 | 513 | 12 | BM901941 | BM901941 |
| C 967 | 18 | 2.9 | 516 | 10 | BG691365 | BG691365 |
| C 968 | 18 | 2.9 | 522 | 9 | AA551312 | AA551312 |
| C 969 | 18 | 2.9 | 522 | 10 | BB867467 | BB867467 |
| C 970 | 18 | 2.9 | 523 | 12 | BM420466 | BM420466 |
| C 971 | 18 | 2.9 | 524 | 12 | BM248749 | BM248749 |
| C 972 | 18 | 2.9 | 525 | 9 | AI083552 | AI083552 |
| C 973 | 18 | 2.9 | 525 | 29 | BZ209427 | BZ209427 |
| C 974 | 18 | 2.9 | 526 | 9 | AA589816 | AA589816 |
| C 975 | 18 | 2.9 | 529 | 9 | AA986635 | AA986635 |
| C 976 | 18 | 2.9 | 529 | 13 | BO832325 | BO832325 |
| C 977 | 18 | 2.9 | 530 | 9 | AV594979 | AV594979 |
| C 978 | 18 | 2.9 | 533 | 14 | CB718562 | CB718562 |
| C 979 | 18 | 2.9 | 534 | 9 | AL635090 | AL635090 |
| C 980 | 18 | 2.9 | 535 | 10 | BF079553 | BF079553 |
| C 981 | 18 | 2.9 | 536 | 9 | AV665904 | AV665904 |
| C 982 | 18 | 2.9 | 536 | 10 | BF551380 | BF551380 |
| C 983 | 18 | 2.9 | 536 | 28 | AZ161317 | AZ161317 |
| C 984 | 18 | 2.9 | 537 | 9 | AA692240 | AA692240 |
| C 985 | 18 | 2.9 | 538 | 9 | AI407899 | AI407899 |
| C 986 | 18 | 2.9 | 538 | 14 | CD421378 | CD421378 |
| C 987 | 18 | 2.9 | 540 | 9 | AA869274 | AA869274 |
| C 988 | 18 | 2.9 | 540 | 12 | BM247898 | BM247898 |
| C 989 | 18 | 2.9 | 541 | 29 | TA200C070 | TA200C070 |
| C 990 | 18 | 2.9 | 542 | 12 | BC969177 | BC969177 |
| C 991 | 18 | 2.9 | 544 | 28 | AZ59983 | AZ59983 |
| C 992 | 18 | 2.9 | 545 | 12 | BI976417 | BI976417 |
| C 993 | 18 | 2.9 | 545 | 28 | AO995499 | AO995499 |
| C 994 | 18 | 2.9 | 545 | 28 | AZ521396 | AZ521396 |
| C 995 | 18 | 2.9 | 545 | 28 | AO527000 | AO527000 |
| C 996 | 18 | 2.9 | 546 | 13 | BO833524 | BO833524 |
| C 997 | 18 | 2.9 | 548 | 10 | BF079230 | BF079230 |
| C 998 | 18 | 2.9 | 548 | 12 | BI499456 | BI499456 |
| C 999 | 18 | 2.9 | 549 | 10 | BB669025 | BB669025 |
| C 1000 | 18 | 2.9 | 552 | 10 | BF519187 | BF519187 |

ALIGNMENTS

RESULT 1
B2862884 765 bp DNA linear GSS 18-MAR-2003
LOCUS CH240_286018.TU CHORI-240 Bos taurus genomic clone CH240_286018,
DEFINITION genomic survey sequence.
ACCESSION B2862884
VERSION B2862884.1 GI:29090289
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 765)

REFERENCE
Zhao,S., Shetty,V., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
A., Gebregorgis,E., Chen,D., Riggs,F., de Jong,P., Crawford,A.M.
and McEwan,J.C.
Bovine BAC End Sequences from Library CHORI-240

TITLE Unpublished
JOURNAL Contact: Shaying Zhao
COMMENT Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaoc@igf.org
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Plietier de Jong (pdejong@mail.cno.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by AgResearch Ltd., New Zealand and The
Institute of Genomic Research (TIGR), USA.
Plate: 286 row: O column: 18
Seg primer: SP6
Class: BAC ends.

FEATURES

source

1..765
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/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_286018"
/sex="Male"
/cell_type="Blood"
/note="vector: pTRABAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 993/5; CHORI-240 Bovine BAC
library (Male) produced by Plietier de Jong"
BASE COUNT 341 a 125 c 122 g 177 t
ORIGIN

Query Match 3.9%; Score 24; DB 29; Length 765;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 356 TTAATTTAAATGAGTAATTTA 379
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Db 142 TTAATTTAAATGAGTAATTTA 165

RESULT 2
CC221787/c 999 bp DNA linear GSS 12-MAY-2003
LOCUS CC221787
DEFINITION CH261-92124.RM1.1 CH261 Gallus gallus genomic clone CH261-92124,
ACCESSION CC221787
VERSION CC221787.1 GI:30546360
KEYWORDS GSS.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 999)

REFERENCE
Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
Unpublished
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@atson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seg primer: RM1 TACGACTCCTCATGAGGAGA
Class: BAC ends
High quality sequence start: 27
High quality sequence stop: 721.

FEATURES

source

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/mol_type="genomic DNA"
/strain="Red Jungle Fowl"

/db_xref="taxon:9031"
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 /clone_lib="CH261"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
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 ordering information: <http://www.chori.org/bacpac>"

BASE COUNT 364 a 185 c 155 g 292 t 3 others

Query Match 3.5%; Score 22; DB 29; Length 999;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 ACTACAAAGGTTTAAATTTA 364
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 Db 838 ACTACAAAGGTTTAAATTTA 817

RESULT 3
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 LOCUS C25646 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
 DEFINITION dictyostelium cDNA clone SSA869, mRNA sequence.
 ACCESSION C25646
 VERSION C25646.1 GI:2281862
 KEYWORDS EST

SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.

REFERENCE 1 (bases 1 to 151)
 Yoshino, R., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M.,
 Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
 The Dictyostelium developmental cDNA project: generation and
 analysis of expressed sequence tags from the first-finger stage of
 development
 JOURNAL DNA Res. 5 (6), 335-340 (1998)
 MEDLINE 99156227
 PUBMED 10048482

COMMENT Contact: Hideko Urushihara
 Institute of Biological Sciences
 University of Tsukuba
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
 Tel: 81-298-53-4664
 Fax: 81-298-53-6614
 Email: hideko@biol.tsukuba.ac.jp
 PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
 POLYA=No.

FEATURES

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 Location/Qualifiers
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 /dev_stage="sling"
 /clone_lib="Dictyostelium discoideum SS (H.Urushihara)"

BASE COUNT 104 a 5 c 6 g 36 t

Query Match 3.4%; Score 21; DB 14; Length 151;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 AGTAAATTTAATATAATAAA 390
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 Db 96 AGTAAATTTAATATAATAAA 116

RESULT 4
 BF761253/c

LOCUS BF761253 461 bp mRNA linear EST 12-JAN-2001
 DEFINITION RC2-CS0017-041000-018-f06 CS0017 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BF761253
 VERSION BF761253.1 GI:12109140
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 461)
 Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL 20202663
 MEDLINE 10737800
 PUBMED
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC2&l2=RC2-CS0017-041000-018-f06&l3=2000-10-04&l4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 79
 High quality sequence stop: 460.

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 /dev_stage="Adult"
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 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORSTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 150 a 99 c 94 g 118 t

Query Match 3.4%; Score 21; DB 10; Length 461;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 GTATATGCTTATTTATTTAT 246
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 Db 64 GTATATGCTTATTTATTTAT 44

RESULT 5
 BF761308/c 462 bp mRNA linear EST 12-JAN-2001

LOCUS BF761308 462 bp mRNA linear EST 12-JAN-2001
 DEFINITION RC2-CS0017-041000-019-f11 CS0017 Homo sapiens CDNA, mRNA sequence.

ACCESSION BF761308
 VERSION BF761308.1 GI:12109195
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 462)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Bordin,S., Costa,P.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE
 PUBLISHED 20020663
 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC2&t2=RC2-CS0017-041000-019-File&t3=2000-10-04&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 38
 High quality sequence stop: 461.

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BASE COUNT 150 a 106 c 96 g 110 t
 ORIGIN

Query Match 3.4%; Score 21; DB 10; Length 462;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 GTATATGCTTATTATTAT 246
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 DB 25 GTATATGCTTATTATTAT 5

RESULT 6
 LOCUS BU482818 469 bp mRNA linear EST 30-NOV-2002
 DEFINITION 603847786f1 CSEQRN22 Gallus gallus cDNA clone CHEST839k22 5', mRNA sequence.
 ACCESSION BU482818
 VERSION BU482818.1 GI:25976395
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Burkarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 1 (bases 1 to 469)
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 JOURNAL MEDLINE
 PUBLISHED 22355534
 12445392

COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source
 1..469
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 /mol_type="mRNA"
 /strain="Layer and broiler"
 /db_xref="taxon:9031"
 /clone="CHEST839k22"
 /sex="Male and female"
 /tissue_type="Chondrocytes isolated from growth plate cartilage"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1lb="CSEQRN22"
 /note="Vector: pBluescript II KS(+); Site: 1: EcoRI; Site: 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT 120 a 114 c 97 g 138 t
 ORIGIN

Query Match 3.4%; Score 21; DB 13; Length 469;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ACAGAGAAAGCAACCCGAA 42
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 DB 88 ACAGAGAAAGCAACCCGAA 108

RESULT 7
 LOCUS AW782526 482 bp mRNA linear EST 30-MAR-2001
 DEFINITION da94b10.x1 Xenopus laevis tadpole stage 24 Xenopus laevis cDNA 3', mRNA sequence.
 ACCESSION AW782526
 VERSION AW782526.1 GI:7797060
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Burkarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.
 1 (bases 1 to 482)
 Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCam,R., Waterston,R. and Wilson,R.
 Washu Xenopus EST project, 1999
 Unpublished
 Contact: Sandy Clifton, Ph.D.
 Washu Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810


```

BASE COUNT      180 a      104 c      122 g      151 t
ORIGIN
Query Match      3.4%; Score 21; DB 13; Length 557;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      156 ACCTCATTTTGAACAATTTT 176
Db      26 ACCTCATTTTGAACAATTTT 46

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LOCUS
DEFINITION
ACCESSION      BU299715
VERSION
KEYWORDS
SOURCE
ORGANISM
Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 600)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22355534
PUBMED
12445392
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES
source
1..600
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton line 15T"
/db_xref="taxon:9031"
/clone="CHEST620j4"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone.lib="CSEQCHN56"
/note="Organ: small intestine; Vector: pBluescript II KS(+)
; Site_1: EcoRI; Site_2: NotI; This normalized library
was constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

BASE COUNT      158 a      148 c      145 g      149 t
ORIGIN
Query Match      3.4%; Score 21; DB 13; Length 600;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      22 ACAGAGAAAGCAACCCGAAA 42
Db      228 ACAGAGAAAGCAACCCGAAA 248

RESULT 11      613 bp      mRNA      linear      EST 29-NOV-2002
BU425547      603230891F1 CSEQRBN09 Gallus gallus cDNA clone CHEST226e23 5', mRNA
LOCUS
DEFINITION
ACCESSION      BU425547
VERSION
KEYWORDS
SOURCE
ORGANISM
Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 613)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22355534
PUBMED
12445392
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES
source
1..613
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST226e23"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone.lib="CSEQRBN09"
/note="Vector: pBluescript II KS(+); Site_1: EcoRI;
Site_2: NotI; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunt-ended, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."

BASE COUNT      164 a      152 c      144 g      153 t
ORIGIN
Query Match      3.4%; Score 21; DB 13; Length 613;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 ACAGAGAAAGCAACCCGAAA 42
Db      226 ACAGAGAAAGCAACCCGAAA 246

RESULT 12

```

BJ066017/c 636 bp mRNA linear EST 10-DEC-2001
 LOCUS BJ066017 NIBB Mochii normalized Xenopus tailbud library Xenopus
 DEFINITION laevis cDNA clone XL084007 5', mRNA sequence.
 ACCESSION BJ066017
 VERSION BJ066017.1 GI:17479068
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 636)
 AUTHORS Kityayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
 Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 FEATURES
 source 1..636
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="XL084007"
 /tissue_type="whole embryo"
 /dev_stage="stage 25"
 /clone_lib="NIBB Mochii normalized Xenopus tailbud
 library"
 BASE COUNT 182 a 135 c 122 g 195 t 2 others
 ORIGIN
 Query Match 3.4%; Score 21; DB 12; Length 636;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 156 ACGTCATTTGAAACAATTTT 176
 ||||||||||||||||||
 Db 592 ACGTCATTTGAAACAATTTT 572
 RESULT 13
 BU291718 642 bp mRNA linear EST 27-NOV-2002
 LOCUS BU291718
 DEFINITION 604164863F1 CSEQCHN55 Gallus gallus cDNA clone CHEST1022m16 5',
 mRNA sequence.
 ACCESSION BU291718
 VERSION BU291718.1 GI:25741174
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 642)
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr Biol. 12 (22), 1965-1966 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 FEATURES
 source 1..642
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="compton line 15T"
 /db_xref="taxon:9031"
 /clone="CHEST1022m16"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN55"
 /note="Organ: Kidney + adrenal; Vector: pBluescript II
 KS(+); Site 1: EcoRI; Site 2: NotI; This normalized
 library was constructed from 1 million independent clones.
 cDNA synthesis was initiated using an oligo(dT) primer.
 Using methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with EcoRI
 , size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."
 BASE COUNT 179 a 175 c 167 g 121 t
 ORIGIN
 Query Match 3.4%; Score 21; DB 13; Length 642;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 ACAGAGAAAGCAACCCGAAA 42
 ||||||||||||||||||
 Db 443 ACAGAGAAAGCAACCCGAAA 463
 RESULT 14
 BU074501/c 649 bp mRNA linear EST 11-DEC-2001
 LOCUS BU074501
 DEFINITION laevis cDNA clone XL090908 5', mRNA sequence.
 ACCESSION BU074501
 VERSION BU074501.1 GI:17504690
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 649)
 AUTHORS Kityayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
 Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 FEATURES
 source 1..649
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="XL090908"
 /tissue_type="whole embryo"
 /dev_stage="stage 25"
 /clone_lib="NIBB Mochii normalized Xenopus tailbud
 library"

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BASE COUNT      182 a      138 c      126 g      197 t      6 others
ORIGIN
Query Match      3.4%; Score 21; DB 12; Length 649;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      156 ACGTCATTTGGAACAATTTT 176
      |||||||
Db      604 ACGTCATTTGGAACAATTTT 584

RESULT 15
BH938769      781 bp      DNA      linear      GSS 01-OCT-2002
LOCUS      odg3ja12.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION
ACCESSION      BH938769
VERSION      BH938769.1 GI:23418935
KEYWORDS
SOURCE
ORGANISM      Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 781)
Delehanthy,K., Fewell,G., Fulton,L., McComble,W.R., Miner,T., Nash
W., Rabhinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished
JOURNAL
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Plate: odg13 row: a column: 12
Seq primer: -28RPPOT reverse
Class: Shotgun
High quality sequence start: 74
High quality sequence stop: 511.
Location/Qualifiers
1.781
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabhinowicz (CSHU) and the
shotgun library prepared at Washington University Genome
Sequencing Center."
BASE COUNT      232 a      212 c      120 g      216 t      1 others
ORIGIN
Query Match      3.4%; Score 21; DB 28; Length 781;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      589 CTAATTCCTATGACAAATTAAT 609
      |||||||
Db      545 CTAATTCCTATGACAAATTAAT 565

RESULT 16
BU382929      821 bp      mRNA      linear      EST 28-NOV-2002
LOCUS      603860114F1 CSEQCHN75 Gallus gallus cDNA clone ChST870K4 5', mRNA
DEFINITION
ACCESSION      BU382929
VERSION      BU382929.1 GI:25890930
KEYWORDS
EST.
SOURCE      Gallus gallus (chicken)

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ORGANISM      Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 821)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Pong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.V.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22355534
MEDLINE
PUBMED
12445392
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
)
PO Box 88, Manchester, M60 1OD, UK
Tel: 0161208930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
1..821
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST870K4"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSEQCHN75"
/note="Organ: trunks; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntend, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
BASE COUNT      217 a      226 c      222 g      156 t
ORIGIN
Query Match      3.4%; Score 21; DB 13; Length 821;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      22 ACAGAGAAAGCAACCCGAAA 42
      |||||||
Db      676 ACAGAGAAAGCAACCCGAAA 696

RESULT 17
A2679224      883 bp      DNA      linear      GSS 14-DEC-2000
LOCUS      ENTMM377R Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION
ACCESSION      A2679224
VERSION      A2679224
KEYWORDS      genomic, genomic survey sequence.
SOURCE      GSS.
ORGANISM      Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE
1 (bases 1 to 883)
Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished
JOURNAL
Contact: Brendan J Loftus
Department of Eukaryotic Genomics

```

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@igf.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence stop: 664.
Location/Qualifiers

1. .883
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOSt; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 384 a 77 c 82 g 340 t
ORIGIN

Query Match 3.4%; Score 21; DB 28; Length 883;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 348 AAAGTTTTTAATTAAATG 368
|||||
Db 116 AAAGTTTTTAATTAAATG 136

RESULT 18 BH135234 927 bp DNA linear GSS 07-AUG-2001
LOCUS BH135234
DEFINITION ENTN54TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
ACCESSION BH135234
VERSION BH135234
KEYWORDS BH135234.1 GI:15094295
SOURCE GSS.
ORGANISM Entamoeba histolytica
REFERENCE 1 (bases 1 to 927)
AUTHORS loftus,B., Wang,Z., Van Aken,S. and Fraser,C.
TITLE Determination of clone end sequences from Entamoeba histolytica
JOURNAL HM1:IMSS sheared DNA library (2001)
COMMENT Unpublished
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@igf.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 27
High quality sequence stop: 592.
Location/Qualifiers

FEATURES
source 1. .927

/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOSt; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 400 a 89 c 113 g 325 t
ORIGIN

Query Match 3.4%; Score 21; DB 28; Length 927;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 348 AAAGTTTTTAATTAAATG 368
|||||
Db 69 AAAGTTTTTAATTAAATG 89

RESULT 19 CNS007PK 942 bp DNA linear GSS 03-JUN-1999
LOCUS CNS007PK/C
DEFINITION Drosophila melanogaster genome survey sequence TE33 end of BAC # BACR15G19 of RPCR-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL067463
VERSION AL067463
KEYWORDS AL067463.1 GI:4946027
SOURCE GSS.
ORGANISM Drosophila melanogaster (fruit fly)
REFERENCE 1 (bases 1 to 942)
AUTHORS Drosophila melanogaster.
TITLE Drosophila melanogaster.
JOURNAL Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
COMMENT Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCR-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers

FEATURES
source 1. .942

/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR15G19"
/clone_lib="RPCR-98"
/note="end : TE33"

BASE COUNT 272 a 169 c 133 g 253 t 115 others
 ORIGIN

Query Match 3.4%; Score 21; DB 29; Length 942;
 Best Local Similarity 100.0%; Pred.No. 36;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 504 AAACCTTTTACCATTAATTA 524
 |||
 Db 199 AAACCTTTTACCATTAATTA 179

RESULT 20 1038 bp DNA linear GSS 12-MAY-2003
 CC226751/c
 LOCUS CH261-4309, Sp6.1 CH261 Gallus gallus genomic clone CH261-4309,
 DEFINITION genomic survey sequence.
 CC226751
 VERSION CC226751.1 GI:30553414
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 1038)
 Krenitki,C., Higgsbotham,J., Wylie,K., Carter,J., McPherson,J.,
 Warren,W., Graves,T., Mardis,E. and Wilson,R.
 TITLE Gallus gallus BAC End Reads
 JOURNAL Unpublished
 COMMENT Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu
 Insert Length: 18200 Std Error: 0.00
 Seq primer: Sp6 ATTAGTGTACACATATAG
 Class: BAC ends
 High quality sequence start: 73
 High quality sequence stop: 568.
 FEATURES
 source location/Qualifiers
 1..1038
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-4309"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: PTARBAC2.1; Site 1: EORI; Site 2: EORI;
 CH261 Female Chicken library - For library and clone
 ordering information: http://www.chori.org/bacpac"
 BASE COUNT 324 a 226 c 198 g 283 t 7 others
 ORIGIN

Query Match 3.4%; Score 21; DB 29; Length 1038;
 Best Local Similarity 100.0%; Pred.No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 354 TTTTAAATTTAATGAGTAA 374
 |||
 Db 978 TTTTAAATTTAATGAGTAA 958

RESULT 21 1101 bp DNA linear GSS 03-JUN-1999
 CNS002YD/c
 LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
 DEFINITION BACR07023 of RPT-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL064229
 VERSION AL064229.1 GI:4941379
 KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazuhiro Osoegawa and
 Aaron Mamoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPT-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 FEATURES
 source location/Qualifiers
 1..1101
 /organism="Drosophila melanogaster"
 /mol_type="Genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR07023"
 /clone_lib="RPT-98"
 /note="end : TET3"
 BASE COUNT 280 a 220 c 202 g 346 t 53 others
 ORIGIN

Query Match 3.4%; Score 21; DB 29; Length 1101;
 Best Local Similarity 100.0%; Pred.No. 38;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 504 AAACCTTTTACCATTAATTA 524
 |||
 Db 201 AAACCTTTTACCATTAATTA 181

RESULT 22 165 bp DNA linear GSS 16-FEB-2001
 A2786231/c
 LOCUS 2M0031D07R Mouse 10kb plasmid UUC2M library Mus musculus genomic
 DEFINITION clone UUCG2M0031D07 R, genomic survey sequence.
 A2786231
 ACCESSION A2786231.1 GI:12923783
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 165)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0031 row: D column: 07
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 165.

FEATURES
 source
 Location/Qualifiers
 1..165

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U08C2M0031D07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid U08C1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb]|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 53 a 24 c 36 g 52 t
 ORIGIN

Query Match 3.2%; Score 20; DB 28; Length 165;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 554 TGCTTAATACAGATAGTA 573
 |||||||
 DB 20 TGCTTAATACAGATAGTA 1

RESULT 23
 A0088456/c

LOCUS
 DEFINITION HS_2208 B1.D03 MF.CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=H, genomic survey sequence.

ACCESSION A0088456
 VERSION A0088456.1 GI:3457367
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE
 JOURNAL Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 MEDLINE Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 PUBMED 10449764

COMMENT
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 2208 row: H column: 5
 Class: BAC ends
 High quality sequence stop: 296.

FEATURES
 source
 Location/Qualifiers
 1..296

/organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=2208 Col=5 Row=H"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelobAC11, BAC clones in E-Coli DH10B"

BASE COUNT 126 a 45 c 42 g 83 t
 ORIGIN

Query Match 3.2%; Score 20; DB 28; Length 296;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 ACAAGGTTTTTAATTAA 365
 |||||||
 DB 181 ACAAGGTTTTTAATTAA 162

RESULT 24
 AV109204

LOCUS
 DEFINITION AV109204 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA
 clone 2600001A05, mRNA sequence.

ACCESSION AV109204
 VERSION AV109204.1 GI:5256752
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 300)

Akchira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara A., Hayatsu,N., Horii,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Suganara Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y., Tomimaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

RIKEN Mouse ESTs
 Unpublished
 TITLE
 JOURNAL
 COMMENT

Contact: Chie Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098

Email: genome-res@tc.riken.go.jp
 Thermostabilization and thermocatalytic activation of thermostable enzymes by
 ThermoStabilization and its application for the synthesis of full length cDNA
 (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.ttc.riken.go.jp) for
 further details.

FEATURES
 source
 Location/Qualifiers
 1..300

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="2600001A05"

```

/sex="mixed"
/dev stage="10-day embryo"
/clone.lib="Mus musculus C57BL/6J 10-day embryo"
BASE COUNT      69 a      57 c      64 g      110 t
ORIGIN
Query Match      3.2%; Score 20; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY      279 AATATTACTTTTATTGCTG 298
      |||||
      60 AATATTACTTTTATTGCTG 79
RESULT 25
LOCUS      AO909076      343 bp      DNA      linear      GSS 09-JAN-2001
DEFINITION      GSSrc07510 Trypanosoma cruzi random genomic library Trypanosoma
ACCESSION      AO909076
VERSION      AO909076
KEYWORDS      AO909076.3 GI:10134221
SOURCE      GSS.
ORGANISM      Trypanosoma cruzi
      Trypanosoma cruzi
      Eukaryota; Elenulozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE      Trypanosoma; Schizocryptanum.
AUTHORS      1 (bases 1 to 343)
      Agniero, F., Verdun, R., Frasch, A. C. C. and Sanchez, D. O.
TITLE      A random sequencing approach for the analysis of the trypanosoma
      cruzi genome: general structure, large gene and repetitive DNA
      families, and gene discovery
      Genome Res. 10 (12), 1996-2005 (2000)
JOURNAL      20568489
MEDLINE      11116094
PUBMED
COMMENT      On Sep 14, 2000 this sequence version replaced gi:925985.
      Contact: Sanchez D. O.
      Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
      San Martin)
      Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
      Aires, Argentina
      Tel: (54-11) 4580/7255/7
      Fax: (54-11) 4752-9639
      Email: dsanchez@lib.unsam.edu.ar
      Sequences were basecalled with phred and vector was masked with
      crossmatch (see http://genome.washington.edu). Sequences were then
      trimmed from both ends to remove low quality bases and masked
      vector.
      Seq primer: T7
      Class: shotgun.
FEATURES
      source
      Location/Qualifiers
          1..343
              /organism="Trypanosoma cruzi"
              /mol_type="Genomic DNA"
              /strain="Cb-Brener"
              /db_xref="raxon:5693"
              /clone="G3IM3"
              /cell_type="epimastigote"
              /clone.lib="Trypanosoma cruzi random genomic library"
              /note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
              randomly sheared using a nebulizer and the 1 to 2 kb range
              was gel purified and cloned into the dephosphorylated
              HindIII site of the vector"
BASE COUNT      130 a      60 c      55 g      98 t
ORIGIN
Query Match      3.2%; Score 20; DB 28; Length 343;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      227 TATATGCTTATTATTAT 246
      |||||
      292 TATATGCTTATTATTAT 273
DB

```

| RESULT 26 | LOCUS | DEFINITION | ACCESSION | VERSION | KEYWORDS | SOURCE | ORGANISM | REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT | | |
|------------|------------|--|------------------------------------|--|-----------------------|--|--|--|--|--|---------------------|---|------|-------|
| B61289 | B61289 | T2109TR TMU Arabidopsis thaliana genomic clone T2109, genomic survey sequence. | B61289 | B61289 | GI:2628051 | GSS. | Arabidopsis thaliana (chale cress) | Rounsley S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wilde,C., Adams,M.D. and Venter ,J.C. | A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3 | Unpublished | Other GSSs: T2109TF | Contact: Steve Rounsley Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: rounsley@igr.org Seq primer: M13 Reverse Class: BAC ends High quality sequence stop: 344. Location/Qualifiers | | |
| FEATURES | source | 1..344 | /organism="Arabidopsis thaliana" | /mol_type="genomic DNA" | /strain="Columbia" | /db_xref="taxon:3702" | /clone="T2109" | /sex="hermaphrodite" | /clone_lib="TMU" | /note="Vector: BelobAC11; Site_1: HindIII; Site_2: HindIII ; Produced by Rod Wing" | 106 a | 50 c | 48 g | 140 t |
| BASE COUNT | ORIGIN | Query Match | 3.2%; Score 20; DB 28; Length 344; | Best Local Similarity | 100.0%; Prod. No. 94; | Matches. 20; Conservative | 0; Mismatches | 0; Indels | 0; Gaps | 0; | | | | |
| OY | 227 | TAATGCTTATTATTAT 246 | | | | | | | | | | | | |
| Db | 74 | TATATGCTTATTATTAT 93 | | | | | | | | | | | | |
| RESULT 27 | BF481067/c | BF481067 | 357 bp | mRNA | linear | EST 05-DEC-2000 | LOCUS | PM1.16 A04.b1 A003 Floral-induced Meristem 1 (FMI) Sorghum | PROINQUUM cDNA, mRNA sequence. | BF481067 | BF481067.1 | GI:11551888 | EST. | |
| ACCESSION | KEYWORDS | Sorghum proinquinum | Sorghum proinquinum | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum. | 1 (bases 1 to 357) | Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and Pratt ,L.H. | An EST database from Sorghum: floral-induced meristems | | | | | | | |

JOURNAL
COMMENT

Unpublished
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp@at@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 310
POLYA=No.

FEATURES
source

Location/Qualifiers

1..357
/organism="Sorghum propinquum"
/mol_type="mRNA"
/db_xref="taxon:132711"
/clone_lib="Floral-Induced Meristem 1 (FM1)"
/note="Organ: Floral-Induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested. The
library was made from poly-A RNA in the cloning vector
lambda Zap II. Clones to be sequenced were prepared by
mass excision."

BASE COUNT
ORIGIN

55 a 137 c 98 g 66 t 1 others

Query Match 3.2%; Score 20; DB 10; Length 357;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 110 CTGCAGCAGGATCTGGGG 129
|||||
Db 236 CTGCAGCAGGATCTGGGG 217

RESULT 28
AW779697/c
LOCUS hns4a01.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3034536 3',
DEFINITION mRNA sequence.
AW779697 364 bp mRNA linear EST 12-MAY-2000
VERSION AW779697.1 GI:7794300
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 364)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN, send email to:
info@image.lnl.gov
Seq primer: -40UP from Gibco.

FEATURES
source

1..364
Location/Qualifiers
/organism="Homo sapiens"

BASE COUNT
ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3034536"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid1"
/note="Organ: Kidney; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

Query Match 3.2%; Score 20; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 183 TATTTTACAGATCATTTTC 202
|||||
Db 77 TATTTTACAGATCATTTTC 58

RESULT 29
AW503250/c

LOCUS vm12f01.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
DEFINITION IMAGE:1020985 3', mRNA sequence.
AW503250 402 bp mRNA linear EST 11-MAR-1999
VERSION AW503250.1 GI:4401101
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 402)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theisling,B., Allen,M., Bowers,Y., Person
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterson,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL
COMMENT Unpublished
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:571761

This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 401.

FEATURES
source

1..402
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:1020985"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:

Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGACGACG 3' ~3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3' "

BASE COUNT

124 a 74 c 76 g 128 t

Query Match 3.2%; Score 20; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 554 TGCTTAATACGAGATAGTA 573
Db 263 TGCTTAATACGAGATAGTA 244

RESULT 30

AV683576

LOCUS 403 bp mRNA linear EST 16-JAN-2002

DEFINITION AV683576 GKC Homo sapiens cDNA clone GKCAF12 5', mRNA sequence.

ACCESSION AV683576

VERSION AV683576.1 GI:10285439

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 403)

Xu X., Huang J., Xu Z., Qian B., Zhu Z., Yan Q., Cai T., Zhang X., Xiao H., Qu J., Liu F., Huang Q., Cheng Z., Li N., Du J., Hu W., Shen K., Lu G., Fu G., Zhong M., Xu S., Gu W., Huang W., Zhao X., Hu G., Gu J., Chen Z., and Han Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

21625106

11752456

CONTACT: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203 P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

Location/Qualifiers

1.403

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="GKCAF12"

/tissue_type="hepatocellular carcinoma"

/dev_stage="Adult"

/lab_host="SOLR"

/clone_id="GKC"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 106 a 81 c 99 g 117 t

ORIGIN

Query Match 3.2%; Score 20; DB 9; Length 403;

Best Local Similarity 100.0%; Pred. No. 97;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 589 CTAATTCATGACAAATTA 608

Db 166 CTAATTCATGACAAATTA 185

RESULT 31

BM200515

403 bp mRNA linear EST 05-NOV-2002

LOCUS

BM200515

403 bp mRNA linear EST 05-NOV-2002

LOCUS

BM200515

403 bp mRNA linear EST 05-NOV-2002

LOCUS

BM200515

403 bp mRNA linear EST 05-NOV-2002

LOCUS

BM200515

403 bp mRNA linear EST 05-NOV-2002

DEFINITION BM200515 Nori Satoh unpublished cDNA library, cleaving embryo Ciona intestinalis cDNA clone c1c1074007 5', mRNA sequence.

ACCESSION BM200515

VERSION BM200515.1 GI:24614944

KEYWORDS EST.

SOURCE Ciona intestinalis

ORGANISM Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 403)

Satou, Y., Shin, I. T., Kohara, Y. and Satoh, N.

Expressed genes in Ciona intestinalis (2002c)

Unpublished

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1.403

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone="c1c1074007"

/tissue_type="whole body"

/dev_stage="cleaving embryo"

/clone_id="Nori Satoh unpublished cDNA library, cleaving embryo"

BASE COUNT 112 a 49 c 76 g 158 t 8 others

ORIGIN

Query Match 3.2%; Score 20; DB 13; Length 403;

Best Local Similarity 100.0%; Pred. No. 97;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 CATTGGAACAAATTTCTA 179

Db 136 CATTGGAACAAATTTCTA 155

RESULT 32

AV806526

LOCUS 410 bp mRNA linear EST 29-MAR-2002

DEFINITION AV806526 RAP19 Arabidopsis thaliana cDNA clone RATL09-46-P03 3',

mRNA sequence.

ACCESSION AV806526

VERSION AV806526.1 GI:19840511

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 410)

Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,

Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,

Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y.

and Shinozaki, K.

Large scale analysis of Arabidopsis full-length cDNA (2002b)

Unpublished

Contact: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: msek@rc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially

as reported previously (Seki et al., 1998). cDNA cleaved with BamHI

and XhoI was ligated to modified lambda PUC-1 vector (Carninci et

al., submitted for publication) digested with BamHI and SalI. This

clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source

Location/Qualifiers

1..410

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="RAFL09-46-P03"

/dev_stage="plants at various developmental stages from germination to mature seeds"

/lab_host="DH10B"

/clone_lib="RAFL9"

/note="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) treatments"

BASE COUNT

131 a 81 c 93 g 105 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 97;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

380 ATATATATTAAGGTTGAAA 399

Db

19 ATATATTAAGGTTGAAA 38

RESULT 33

LOCUS

AO683917 443 bp DNA linear GSS 28-JUN-1999

DEFINITION

HS 5455 B2_E10 SP6E RPT-11 Human Male BAC Library Homo sapiens genomic clone Plate=1031 Col=20 Row=D, genomic survey sequence.

ACCESSION

AO683917

VERSION

AO683917.1 GI:5259900

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 443)

AUTHORS

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE

99380589

COMMENT

10449764

JOURNAL

Contact: Mahairas GG, Wallace JC, Hood L

MEDLINE

High Throughput Sequencing Center

COMMENT

University of Washington

JOURNAL

401 Queen Anne Avenue North, Seattle, WA 98109, USA

MEDLINE

Tel: (206) 616-3618

COMMENT

Fax: (206) 616-3887

JOURNAL

Email: jwallace@u.washington.edu

MEDLINE

Clones are derived from the human BAC library RPT-11. For BAC

COMMENT

library availability, please contact Pieter de Jong

JOURNAL

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

MEDLINE

BACAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

COMMENT

or from Research Genetics (<http://www.resgen.com>). BAC end Web Server:

JOURNAL

<http://www.htsc.washington.edu>

MEDLINE

Plate: 1031 row: J column: 20

COMMENT

Seq primer: SP6

JOURNAL

Classes: BAC ends

MEDLINE

High quality sequence stop: 443.

COMMENT

Location/Qualifiers

FEATURES

source

1..443

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=1031 Col=20 Row=J"

/sex="male"

/clone_lib="RPT-11 Human Male BAC Library"

/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

BASE COUNT

132 a 104 c 95 g 112 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 98;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

.232 GCTTATTATTATGTTGC 251

Db

118 GCTTATTATTATGTTGC 99

RESULT 34

LOCUS

BF871659 467 bp mRNA linear EST 17-JAN-2001

DEFINITION

OVO-ET0150-011100-467-b06 ET0150 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF871659

VERSION

BF871659.1 GI:12261789

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 467)

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsumura,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

TITLE

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

JOURNAL

Shotgun sequencing of the human transcriptome with ORF expressed

MEDLINE

sequence tags

COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

20202663

MEDLINE

10737800

COMMENT

Contact: Simpson A.J.G.

JOURNAL

Laboratory of Cancer Genetics

MEDLINE

Ludwig Institute for Cancer Research

COMMENT

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

JOURNAL

Tel: +55-11-2704922

MEDLINE

Fax: +55-11-2707001

COMMENT

Email: asimpson@ludwig.org.br

JOURNAL

This sequence was derived from the FAPESP/LICR Human Cancer Genome

MEDLINE

Project. This entry can be seen in the following URL

COMMENT

(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV0&ct2=QV0-ET0150-011100-467-b06&ct3=2000-11-01&ct4=1>)

JOURNAL

Seq primer: puc 18 forward

MEDLINE

High quality sequence start: 51

COMMENT

High quality sequence stop: 377.

JOURNAL

Location/Qualifiers

FEATURES

1..467

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="Adult"

/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;

JOURNAL

Site 2: SmaI; A mini-library was made by cloning products

MEDLINE

derived from ORESTES PCR (U.S. Letters Patent application

COMMENT

No. 196,716 - Ludwig Institute for Cancer Research)

JOURNAL

profiles into the pUC 18 vector. Reverse transcription of

MEDLINE

tissue mRNA and cDNA amplification were performed under

COMMENT

low stringency conditions."

JOURNAL

140 a 103 c 121 g 103 t

BASE COUNT

ORIGIN

Query Match 3.2%; Score 20; DB 10; Length 467;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 ATGCTTATTATTATGTT 249
 |||||
 408 ATGCTTATTATTATGTT 389

RESULT 35
 A0052026 481 bp DNA linear GSS 20-APR-1999
 LOCUS RPICT11-49024.TV RPICT-11 Homo sapiens genomic clone RPICT-11-49024,
 DEFINITION genomic survey sequence.
 ACCESSION A0052026
 VERSION A0052026.1 GI:3349063
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 481)
 Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
 Venter,J.C.
 Venter,J.C.
 Use of BAC End Sequences for Sequence-Ready Map Building (1998)
 TITLE Unpublished
 JOURNAL
 COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are derived from the human BAC library RPICT-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@edlong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (http://resgen.com). BAC end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
 Class: BAC ends.
 FEATURES
 Location/Qualifiers
 1..481
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GBS:7518791"
 /db_xref="taxon:9606"
 /clone="RPICT-11-49024"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPICT-11"
 /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
 RPICT11 Human Male BAC library"
 BASE COUNT 169 a 92 c 120 g 100 t
 ORIGIN

Query Match 3.2%; Score 20; DB 28; Length 481;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 CTCAGAGATAGCTATTTTA 270
 |||||
 394 CTCAGAGATAGCTATTTTA 413

RESULT 36
 A2450611 482 bp DNA linear GSS 04-OCT-2000
 LOCUS A2450611
 DEFINITION 1M0249K19F Mouse 10kb plasmid UNGC1M library Mus musculus genomic
 clone UNGC1M0249K19 F, genomic survey sequence.
 ACCESSION A2450611
 VERSION A2450611.1 GI:10605573
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 482)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0249 row: K column: 19
 Seq primer: CGTTGTAAACGACGCCACAGT
 Class: plasmid ends
 High quality sequence stop: 482.
 FEATURES
 Location/Qualifiers
 1..482
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UNG1M0249K19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UNGC1M library"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD43 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 BASE COUNT 137 a 99 c 87 g 159 t
 ORIGIN

Query Match 3.2%; Score 20; DB 28; Length 482;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 233 CTTTATTATTATGTTGCT 252
 |||||
 399 CTTTATTATTATGTTGCT 418

RESULT 37
 B2861579 483 bp DNA linear GSS 18-MAR-2003
 LOCUS B2861579
 DEFINITION CH240_258J20.TV CHORI-240 Bos taurus genomic clone CH240_258J20,
 genomic survey sequence.
 ACCESSION B2861579
 VERSION B2861579.1 GI:29089384

KEYWORDS
SOURCE GSS.
ORGANISM Bos taurus (cow)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS 1 (bases 1 to 483)
 Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Chen, D., Riggs, F., de Jong, P., Crawford, A.M. and McEwan, J.C.
 Bovine BAC End Sequences from Library CHORI-240
 Unpublished
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@tigr.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by AgResearch Ltd., New Zealand and The Institute of Genomic Research (TIGR), USA.
 Plate: 258 row: J column: 20
 Seq primer: T7
 Class: BAC ends.

FEATURES
source Location/Qualifiers
 1..483
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="Breed: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_258J20"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="Vector: pTRABAC1.3; Site_1: MboI; Site_2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

BASE COUNT
 184 a 69 c 73 g 157 t

ORIGIN

Query Match 3.2%; Score 20; DB 29; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 159 TCATTTCGAACAAATTTCT 178
 |||||
 24 TCATTTCGAACAAATTTCT 43

RESULT 38
LOCUS BF889646 491 bp mRNA linear EST 25-APR-2001
DEFINITION 289193 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF889646
VERSION BF889646.1 GI:12281104
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS 1 (bases 1 to 491)
 Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Caeas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Perle, G., Holt, I., Karayancheva, S., Liang, F., Quackenbush, J. and Keefe, J.W.

TITLE
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978

COMMENT
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@meat.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 PCR primers
 FORWARD: AGGAAACGATGACCAT
 BACKWARD: GGTTCCTCCAGTCACGACG
 Plate: 94 row: M column: 24
 Seq primer: ATTAGGTGACACTATAG.
 Location/Qualifiers
 1..491
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /rname_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 3BOV"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

BASE COUNT
 151 a 78 c 96 g 166 t

ORIGIN

Query Match 3.2%; Score 20; DB 10; Length 491;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 348 AAAGCTTTTAAATTAAT 367
 |||||
 381 AAAGCTTTTAAATTAAT 400

RESULT 39
LOCUS BP956275/c 498 bp mRNA linear EST 22-JAN-2001
DEFINITION QV2-NN0045-211100-495-F02 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BP956275
VERSION BP956275.1 GI:12373550
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 498)
 Dias Neto, E., Garcia Correa, R., Verjovskij-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 2020263
PUBMED 10737800

COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV2&t=QV2-NN0045-21100-495-02&t3=2000-11-21&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 14
 High quality sequence stop: 498.
 Location/Qualifiers
 1..498
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NN0045"
 /note="Organ: nervous normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 178 a 68 c 92 g 160 t
 ORIGIN

Query Match 3.2%; Score 20; DB 10; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 AACCAATTTCTACTATATTT 187
 |||||
 Db 373 AACCAATTTCTACTATATTT 354

RESULT 40
 BE721612 498 bp mRNA linear EST 25-APR-2001
 LOCUS 189200 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION BE721612
 ACCESSION BE721612
 VERSION BE721612.1 GI:10122908
 KEYWORDS EST.
 SOURCE
 ORGANISM Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.
 1 (bases 1 to 498)
 Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,W.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perlea,G., Holt,I., Karaycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.

REFERENCE
 AUTHORS
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 21180013
 11282978
 Contact: Smith TPJ
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
 PCR primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACGACGACG
 Plate: 40 row: K column: 12
 Seq primer: ATTAGGTGACACTATAG.
 Location/Qualifiers
 1..498

FEATURES
 source

/organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 2BOV"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
 BASE COUNT 157 a 90 c 89 g 162 t
 ORIGIN

Query Match 3.2%; Score 20; DB 10; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 AAGGTTTTTAATTAAAT 367
 |||||
 Db 137 AAGGTTTTTAATTAAAT 156

Search completed: October 8, 2003, 07:52:03
 Job time : 1984 secs